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CO524463	CN010050	CO533588	CC710318	CA292935	BM333529	CL960237	BM075490	BM073319	BM376711	BM500306	BE356185	CF428085	CA233892	CA692850	CA243768	BI954597	CA151962	CL297228	CA273712	BH874076
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ALIGNMENTS

RESULT 1 CF326660 LOCUS ORIGIN FEATURES COMMENT REFERENCE SOURCE ORGANISM KEYWORDS VERSION ACCESSION DEFINITION TITLE AUTHORS source Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Le Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H. Large-scale Sequencing Analysis of Rice ESTs Unpublished (2003) Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Eukaryota, Viridiplantae; Streptophyta; Embryophyt
Spermatophyta; Magnoliophyta; Liliopsida; Poales;
Ehrhartoideae; Oryzeae; Oryza. JMT1--06-K20.gl AtJMT-overexpressing transgenic rice lambda phage cDNA library (JMT1) Oryza sativa (japonica cultivar-group) cDNA clone JMT1--06-K20, mRNA sequence.

CF326660 Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, MyongJi University Contact: Nahm B.H. CF326660.1 GI:33801577 Yongin, Kyeonggi, Korea (bases 1 to 478) 82 31 330 6193 82 31 321 6355 /cullivar="Nackdong"
//db xref="taxon:39947"
//clone="JMT1-06-K20"
//tissue_type="leaf"
//dev_stage="14 days after germination"
//lab_host="E.coli SOLR"
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//note="Vector: pBluescript SK(+); Site_1: EcoRI; Site_2: Xhot="Vector: pBluescript SK(+); Site_1: EcoRI; Site_2: Xhot="Vector: and 3' end with XhoI site. mRNA was prepared from Arabidopsis Jasmoinate Carboxyl methyltransferase overexpression line." bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr /organism="Oryza sativa (japonica cultivar-group)" |mol_type="mRNA" ocation/Qualifiers . .478 Embryophyta; Tracheophyta; Lee, T.H., Shin, Y.C., Poaceae; υ

Query Match Best Local Similarity

33.6%;

Score 447; DB 7; Pred. No. 4.2e-87;

Length 478;

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TITLE
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COMMENT
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Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;

Spermatoideae; Oryzeae; Oryza.

1 (bases 1 to 461)

Kim,H., Yu,Y., Wissotski,M., Yost,D., Stum,D., Rao,K., Luo,M.,

Jettty,R., Kudrna,D., Muller,C., Hatfield,J., Soderlund,C. and
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OR_CBa0004J23.f OR_CBa Oryza
5', genomic survey sequence.
CL794965
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Seq primer: TAA TAC GAC TCA CTA TAG
Class: BAC ends.
                                                                                                                                                                                             Arizona Genomics Institute
University of Arizona
Forbes Building Room 303, 7
Tel: 520 626 9595
Fax: 520 621 1259
                                                                                                                                                                                                                                                                                    OMAP project
Unpublished
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                                                                                                                                                                                 Email: http://genome.arizona.edu
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/db_xref="taxon:4529"
/clone="OR_CBa0004J23"
               /mol_type="genomic DNA"
/db_xref="taxon:4529"
                                           organism="Oryza rufipogon"
                                                                           Location/Qualifiers
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1 (bases 1 to 689)

1 Anderson,O.D., Chao,S., Close,T.J., Crossman,C., Fenton,R.D., Lazo,G.R., Nguyen,H.T., Rausch,C.J., Wilson,C., Woo,J. and Zhang,D. The structure and function of the expressed portion of the wheat genomes - Unstressed root cDNA library

Unpublished (2002)
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WHE3514 C07 E14ZS Wheat unstressed root cDNA library
aestivum cDNA clone WHE3514_C07_E14, mRNA sequence.
BQ483926
                                                                                         Contact: Olin Anderson
US Department of Agriculture, Agriculture Research
West Area, Western Regional Research Center
Sequences have been trimmed quality sequence with phred
                                                           800 Buchanan Street,
Tel: 5105595773
                                                                                                                                                                                                                                                                                      Triticum aestivum (bread wheat)
Triticum aestivum
                            Email: oandersn@pw.usda.gov
                                                Fax: 5105595818
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/dev_stage="2 week old seedlings"
/lab_host==DH10B T1 phage resistant"
/clone_lib="VR_CBa"
/note="Vector: pAGIBAC1; Site_1: HindIII;
drk treated 36 hrs before harvest"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Contact: Rod A. Wing
Arizona Genomics Institute
University of Arizona
Porbes Building Room 303, Tucson, AZ 85721-0036, USA
Tel: 520 626 9595
Fax: 520 621 1259
Email: http://genome.arizona.edu
PCR PRimers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FORWARD: TAA TAC GAC TCA CTA TAG GG
BACKWARD: CAC TCA TTA GGC ACC CCA
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Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
1 (bases 1 to 359)
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Kudrna, D., Muller, C., Hatfield, J., Soderlund, C. and Wing, R
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                           TCTCACTAATGTAAACATACATAGATCAGATGCCAAGAGTGCAGGGATTGGGGATTAAAG 1117
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/tlssue_type="young_leaves"
/tlsb_host="DH10B-T1 phage_resistant"
/lab_host="DH10B-T1 phage_resistant"
/clone_lib="OR_BBa"
/note="Vector: pAGIBAC1; Site_1: HindIII; Site_2:
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/db_xref="taxon:4529"
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Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Bukaryota; Varidiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD

Spermatophyta; Magnoliophyta; Liliopsida; Carcharum officinaru
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5', mRNA sequence.
CA185031
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Email: parruda@unicamp.br
Clone distribution: clone distribution
through the Brazilian Clone Collection
http://www.bcccenter.fcav.unesp.br
Plate: 096 row: H column: 06
Seq primer: T7 Promoter Primer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Universidade Estadual de Campinas
Caixa Postal 6010, 13083-970, Campinas
Tel: 55 19 3788 1137
Fax: 55 19 3788 1089
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Vettore, A.L., da Silva, F.R., Kemper, E. The libraries that made SUCEST Genet. Mol. Biol. 24 (1-4), 1-7 (2001)
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GGCGGAGCAGGAGAGGCCAAGGGCATCCCATGGACGGAGGAAGAGCACAGGCTGTTC-T 476
                               CCCACGCAAAAACGGAAAAGACGGCCGCCGCCGGCGTTAACGCGGGGAAGAGTGCTTCTAA
                                                              GAGCCGGAGCCGCCGCCGCCGTCCAA------
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                                                                                                                                                                                                                                   Conservative
                                                                                                                                                                                                                                                                                                               /clome_lib="ST3"
/note="Torgan: Fourth apical stalk internodes of adult /note="Torgan: Fourth apical stalk; Site_2: NotI; An plants; Vector: pSportI; Site_1: SalI; Site_2: NotI; An unidirectional cDNA library generated from [Fourth apical stalk internodes of adult plants]. cDNA was prepared from polyA+ mRNA using SuperScript Plasmid System Kit (Invitrogen). The double-strand cDNAs were fractionated in a sepharose CL-2B 40cm-columns and fragments sizing between 0.8 and 1.5 Kb were directionally cloned into the vector. Details of each source of RNA and library construction can be obtained at http://sucest.lad.ic.unicamp.br/public"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /moltype="mkNA
/db_xref="taxon:4547"
/clone="SCSBST3096H06"
/lab_host="DH10B"
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                                                                                                                                                Arizona Genomics Institute
University of Arizona
Forbes Building Room 303, To
Tel: 520 626 9595
Fax: 520 621 1259
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OR_BBa0098B05.f (
5', genomic surve
                                                                                                                                                                                                                                                                                  Oryza rufipogon

Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;

Spermatoideae; Oryzeae; Oryza.

I (bases 1 to 618)

Kim,H., Yu,Y., Stum,D., Yost,D., Rao,K., Luo,M., Jetty,R.,

Kudrna,D., Muller,C., Hatfield,J., Soderlund,C. and Wing,R.
                           FORWARD: TAA TAC GAC TCA CTA TAG (
BACKWARD: CAC TCA TTA GGC ACC CCA
INSERT Length: 161 Std Error: 0.
Plate: 0098 row: B column: 05
Seg primer: TAA TAC GAC TCA CTA TA
                                                                                                                                                                                                                                   OMAP Project
Unpublished (2004)
Contact: Rod A. Wing
                 Class: BAC ends.
                                                                                                                                                                                                                                                                                                                                                                                                                       CL782098.1
GSS.
                                                                                                                                Email: http://genome.arizona.edu
                                                                                                                  PCR PRimers
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AUTHORS
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Best Local Similarity 97.8%;
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Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnollophyta; Liliopsida; Poales; Poaceae; PACCAD

clade; Panicoideae; Andropogoneae; Zea.

1 (bases 1 to 884)

Whitelaw, C.A., Quackenbush, J., Van Aken, S., Utterback, T.,

Resnick, A., Fraser, C.M., Budiman, M.A., Bedell, J.A., Rohlfing, T.,

Citek, R.W., Nunberg, A., Robbins, D. and Lakey, N.

Consortium for Malze Genomics

Unpublished (2002)

Other GSSs: GGXCQ48TV

Contact: Cathy Whitelaw
                                                                                                                                                                                                                                                                                                                                                                                                             OGXCQ48TH ZM_0.7_1.5_KB Zea
genomic survey sequence.
                                                                                                                                                                                                                                                                                                                                                                                 genomic survey sequence
CG257740
CG257740.1 GI:34164524
                                                                                      Seq
                                                                                                     Email: whitelaw@tigr.org
                                                                                                                                                                                                                                                                                                                                                      Zea mays
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                                                                                       primer: TR
                                                                                                                                                Medical Center Drive,
                                                                                                                    301-838-0208
                                                                                                                                   301-838-5843
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/md_type="genomic DNA"
/db xref="taxon:4529"
/clone="OR_BBa0098B05"
/tissue_type="young leaves"
/lab_host="DH10B-T1 phage resistant"
/clone_lib="OR_BBa"
/note="Vector: pAGIBAC1; Site_1: HindIII; Si
   /organism="Zea mays"
/mol_type="genomic DI
/strain="B73"
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/clone="zMMBMa0650G23"
/clone_lib="ZM_0.7_1.5_KB"
/clone_Tib="ZM_0.7_1.5_KB"
/note="Vector: pBCSK-; Site_1: HincII; 0.7-1.5
methylation filtered genomic DNA library"
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                              GI:32115087
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Pred. No. 2.3e-49;
D; Mismatches 96
                                                                     689 bp DNA
Zea mays genomic
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ZMMBMa0145F04,
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(bases 1 to 689)

Whitelaw, C.A., Quackenbush, J., Van Aken, S., Utterback, Resnick, A., Fraser, C.M., Budiman, M.A., Bedell, J.A., Rocitek, R.W., Nunberg, A., Robbins, D. and Lakey, N. Consortium for Maize Genomics
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Unpublished (2002)
Other_GSSs: OGDAH26TM
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Class: sheared
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Contact: Cathy Whitelaw
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GATTTGTTCTTTGTGTAGTCGCCGGCTCATCGTCCCTGATCATCTTGTTCTCAC
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                                                           ACGCGCCATGGACGG-ACATGAGCAGCATTTCTTCCTCCTCCTTTCTTGATGTCAATCTT
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                                         - CACGCGCCGTACGTCGTGCCCGTCGGCTACCCGGCGCTCCGGCCAAGATGCACCAATG
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301-838-0208
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1. .689
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/clone=1ib="ZM_0.7_1.5_KB"
/note="Vector: pBCSK-; Site_1:
methylation filtered genomic DI
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/mol_type="genomic DI
/strain="B73"
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71.9%;
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Pred. No. 3.1e-47;
0; Mismatches 134;
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Query Match
Best Local Similarity
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1 (bases 1 to 804)

Whitelaw, C.A., Quackenbush, J., Van Aken, S., Utterback, T., Whitelaw, C.A., Budiman, M.A., Bedell, J.A., Rohlfin Citek, R.W., Numberg, A., Robbins, D. and Lakey, N.
Consortium for Maize Genomics
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Other_GSSs: OGWAM96TH
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Email: whitelaw@tigr.org
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Tel: 301-838-5843
Fax: 301-838-0208
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Contact: Cathy Whitelaw
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  CGCCGGCCACATGGT---
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                                                               -----CGGTTCCGCCGATGGGCATGTACGGGCACGCCCCATGGGCCACCCGGT
                                                                                       CCCGGGCGGCGCCCCATGCCCATGTACAGCGCCGCCCATGGGCCACCCGT
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/clone_lib="ZM_0.7_1.5_KB"
/note="Vector: pBCSK-; Site_1: HincII; 0.
methylation filtered genomic DNA library"
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/strain="B73"
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No. 1.:
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Consortium for Maize Genomics
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OG1CL41TH ZM_0.7_1.5_KB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Unpublished (2002)
Other_GSSs: OGICL41TV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      genomic survey sequence CG362076
                                                                                                                                                                                                                                                                                                                                                                                                                                             Email: whitelaw@tigr.org
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Contact: Cathy Whitelaw
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       clade; Panicoideae; Andropogoneae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CG362076.1 GI:34279343
 CACCGCCGGCGATCAGGTCGCCGGCAGCAGGGCGCCGGATCACCGGCCACCAGGCCAC
                                                           CCGCCTCAACTCCATGAACCGCCGACGCCCGCCGCCGCCACCACCACCATCACCAGCGT
                                                                                                              CAACTTCGTCATCTCGCGGACGCCAACGCAGGTGGCGAGCCACGCGCAGAAGTACTTCAT
                                                                                                                                                     CAGGTTGTTCTTGTTGGGTCTGGACAAGTTCGGCAAGGGCGACTGGCGGAGCATCTCGCG
                                                                                                                                                                    CAGGCTGTTCTTGCTGGGGCTGGACAAGTTCGGCAAGGGGGACTGGCGGAGCATCTCGCG
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                                                                                                CAACTTCGTCATCTCGCGGACGCCGACGCAGGTGGCGAGCCCACGCGCAGAAATACTTCAT
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                                                                                                                                                                                                           Conservative
                                                                                                                                                                                                                                                                     /organism="Zea mays"
/mol type="genomic DNA"
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/clone_lb="zwmBMa0730H10"
/note="Vector: pBCSK-; Site_1: HincII; 0.7-:
methylation filtered genomic DNA library"
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74.9%;
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Pred. No. 1.1e-46;
0; Mismatches 103
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CAGGCTGTTCTTGCTGGGGCTGGACAAGTTCGGCAAGGGGGACTGGCGGAGCATCTCGCG 525
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Query Match
Best Local Similarity
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Zea mays
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Resnick,A., Fraser,C.M., Budiman,M.
Citek,R.W., Numberg,A., Robbins,D.
Consortium for Maize Genomics
Unpublished (2002)
Other_GSSs: OGIAD74TV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Whitelaw, C.A., Quackenbush, J., Van Aken, S., Utterback, T., Resnick, A., Fraser, C.M., Budiman, M.A., Bedell, J.A., Rohlfing, T., Citek, R.W., Nunberg, A., Robbins, D. and Lakey, N.
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1 (bases 1 to 933)
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CG219911
CG219911.1 GI:34119799
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CG1AD74TH ZM_0.7_1.5_KB Zea mays
                                                                                                                                                                                                                                                                                                                                                                                                    Email: whitelaw@tigr.org
                                                                                                                                                                                                                                                                                                                                                                                                                               Fax: 301-838-0208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Contact: Cathy Whitelaw
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                                                                                                         /db_xref="taxon:4577"
/clone="zwMBMa0715N04"
/clone="zwMBMa0715N04"
/clone="berzm 0.7 1.5 KB"
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/mol_type="genomic DNA"
/strain="B73"
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Score 262.2; DB 9;
Pred. No. 1.1e-46;
0; Mismatches 103;
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ZMMBMa0715N04,
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                                                                                                Contact: Chen Chen
Department of Bioinformatic
Beijing Institute of Genomics
Chinese Academy of Sciences, Be
Tel: 86-10-80481559
Fax: 86-10-80488676
                                                                                                                                                                                                                                                                  Oryza sativa (indica cultivar-group)
Oryza sativa (indica cultivar-group)
Oryza sativa (indica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
                                                                           Rice
                                                                                                                                                                          Ma,L., Wangc,J., Chen,C., Liu,X., Su,N., Li,L., Wang,X., Cao Jiao,Y., Sun,N., Zhang,X., Bao,J., Sun,D., Zhao,H., Yuan,L., Wong,G.K.S., Deng,X.W. and Wang,J.

An analysis of transcriptional regulation of the rice genome its comparison to Arabidopsis
Unpublished (2004)
                                                                                                                                                                                                                                                                                                                                             cultivar-group) genomic,
CL968676
CL968676.1 GI:52391986
                                                                                                                                                                                                                                                                                                                                                                                CL968676 807 bp DNA linear GSS
OsIFCC017023 Oryza sativa Express Library Oryza sativa
                                                                                      Email: chenchen@genomics.org
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                                                                          genomic sequence.
                                                               exon-trapped
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/mol_type="genomic DNA"
/db_xref="taxon:39946"
                                               Location/Qualifiers
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Sequencing of the maize geno Unpublished (2003)
Contact: Rod Wing Arizona Genomics Institute University of Arizona Biological Sciences West, 44 85721-0088, USA
                                                             BACKWARD: M13r
Plate: 0133 row: 0
Seq primer: M13r
Class: BAC ends.
                                                                                                                                                                                                                                                                                                                                                                                                                             Zea mays
Zea mays
                                                                                                                                                                                                                                                                                                                                                                                                                                                           genomic survey sequence. CC751932 CC751932.1 GI:32211515 GSS.
                                                                                                                                                                             85721-0088, USA
Tel: 520 626 3967
Fax: 520 621 9288
                                                                                                                                                                                                                                                                                                                            and Wing, R.
                                                                                                                                                                                                                                                                                                                                                          Eukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopaida; Poales; Poaceae; PACCAD clade; Panicoideae; Andropogoneae; Zea.

1 (bases 1 to 740)
                                                                                                                                                               Email: http://genome
                                                                                                                                                                                                                                                                                                                                             Yu, Y., Kim, H.R.,
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/note="Oryza sativa exon trapped
/organism="Zea mays"
/mol_type="genomic D
                            1. .740
                                                 Location/Qualifiers
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1 (bases 1 to 468)
Dong, H.T., Li,D.B., Zhuang, X.F., Dai, C.G., Wu,H.F., Jiang, Y.X., Yu,F.C., Gao, Q.K. and A Gene Expression Screen in Oryza sativa Unpublished (2001)
Contact: Haitao Dong, Debao Li
                                                                                                                                                                                           BM038003 468 bp mRNA U001D12 Oryza sativa mature leaf library sativa cDNA clone U001D12, mRNA sequence.
                                                                               Eukaryota; Viridiplantae; Streptophyta; Er
Spermatophyta; Magnoliophyta; Liliopaida;
Ehrhartoideae; Oryzeae; Oryza.
                                                                                                                           Oryza sativa
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/note="Vector: pBeloBAC11; Site_1: HindIII; Site_2:
HindIII; Zea mays L. ssp. mays"
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/db_xref="taxon:4577"
/clone="ZMMBBb0133C24"
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Pred. No. 4.4e-45;
0; Mismatches 108;
                                                                                             Embryophyta; Trach
a; Poales; Poaceae;
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induced by
                                          Sun, L.X.,
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Arizona Genomics Institute
University of Arizona
Biological Sciences West, 44
85721-0088, USA
Tel: 520 626 3967
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Zea mays
                                                                 Yu,Y., Kim,H.R., Hatfield,J.,
and Wing,R.
Sequencing of the maize genome
Unpublished (2003)
Contact: Rod Wing
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                                                                                                                                           Eukaryota; Viridiplantae; Streptophyta; Em
Spermatophyta; Magnoliophyta; Liliopsida;
clade; Panicoideae; Andropogoneae; Zea.
1 (bases 1 to 653)
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Kaixuan Road 268#, Hangzhou,
Tel: 0086-571-86892051
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Seg primer: M13 forward primer.
Location/Qualifiers
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/clone_lib="Oryza sativa mature leaf library induced
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Email: http://genome.arizona.edu
pCR PRimers
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ilarity 73.8%;
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Claim 18; SEQ ID NO 1; 22pp; English.

The invention relates to a pure polypeptide comprising a fully defined Myb protein transcription factor OsMYBS1, OsMYBS2 or OsMYBS3 protein sequence, where the polypeptide regulates expression of a gene in a cell.

DR P-PSDB; XX PT Novel M; PT OsMYBS2 PT cell, pi			•	PF 3							2		200 Tins		4.4. U 4.0	44	4.4	40	א נע	ųψ	36	ω w	ω (3 3 3 1	30	221	22	2 2	N :	22	!
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			.*	·			ion/Qualifiers 940 = a uct= "OsMYBS1"		plant; transgenic; My	JA.			30 Bp.	ALIGNMENTS	ACN54935 ADQ06567	ACN46091	AAC56528	AAC57318	AAC56944	ADO00778	AD000781	ADR60712	ADI44406	AAC47819 ADD29992	AD003516	ADE37148	ABK65370 ADD30950	ADF38031	33	AAC57273 AAC56101	
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The polypeptide is useful for regulating expression of a gene in a plant cell, preferably rice or barley cell. The method is useful for identifying a compound that modulates the activity of the polypeptide. An antibody to the polypeptide is useful for detecting the presence and distribution of OsMYBS proteins in tissues and in cellular compartments and for verifying the expression of OsMYBS proteins in a transgenic plant. Nucleic acid encoding the polypeptide is useful for generating a transgenic plant or producing to determine whether an OsMYBS mRNA is expressed in a tissue or cell. Nucleic acid encoding the polypeptide is also useful as primers in PCR-based detection methods, or as labelled probes in nucleic acid blots (e.g. Northern blots). The compound identified by the method is useful for enhancing or repressing the expression of a gene regulated by the polypeptide, e.g. alpha-amylase gene. The present sequence represents cDNA encoding the rice Myb protein
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99US-0128714P

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25-OCT-1999;
25-OCT-1999;
25-OCT-1999;
26-OCT-1999;
26-OCT-1999;
26-OCT-1999;
                                                                                 New substantially purified nucleic acid molecule that encodes a cotton protein or its fragment, useful as molecular tool for the targeting and isolation of novel genes for plant protection and improvement.
                                        Claim 1; SEQ ID NO 2606; 30pp; English.
                                                                                                                                                                                    WPI; 2004-479807/45
                                                                                                                                                                                                                                  Fincher
                                                                                                                                                                                                                                                                                                                           10-DEC-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           plant improvement; marker-assisted breeding.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Cotton;
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99US-0161361P.
99US-0161920P.
99US-0161992P.
99US-0161993P.
99US-0162142P.
                                                                                                                                                                                                                                                                                                                              99US-0170255P.
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99US-0161404P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 135.4; DB 3; Pred. No. 8.1e-13; 0; Mismatches 76;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ВP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              plant protection;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 1161;
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CC that encodes a cotton protein or its fragment comprising an EST CC (expressed sequence tag) appearing as ADP99999. ADP95919. Also included are a substantially purified cotton protein or its fragment encoded by a CC inclaic acid molecule above and a transformed plant (having a nucleic acid molecule which comprises: an exogenous promoter region which CC functions in a plant cell to cause the production of a mRNA molecule; a CC structural nucleic acid molecule comprising one of the ESTs or their CC cell to cause termination of transcription and addition of polyadenylated CC ribonucleotides to 3' end of the mRNA molecule). The ESTs are useful as CC molecular tool for the targeting and isolation of novel genes for plant CC pathways, for isolating genes and promoters, for identifying and mapping CC determining gene function. The cotton nucleic acid molecules are useful as molecular tags to isolate genesic regions, isolate genes, map genes, and determining if genes are members of a particular gene family and for use in marker-assisted breeding programs. The present sequence is one of the CC 4930 cotton ESTs of the invention. NOTE: The sequences are not displayed on the specification but are available in electronic format from the
                                                    at
                                                 seqdata.uspto.gov/sequence.html?DocID=20040123338
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Sequence 412 BP; 120 A; 83 C; 106 G; 102 T; 0 U; 1 Other;

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                                                                                                                                                                                                                                                                                            Best Local Similarity Matches 192; Conserv
                                                                                                                                                                                                                                                                                                                        Query Match
                                                                                                                                               516
365
                            635
                                                         305
                                                                                                                245
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                                                                                                                                                                                                                                    125
                                                                                                                                                                                                                                                                 396
                                                                                                                                    ACGCCGCAAGAGCTGCTCCAAGGCGGAGCAGGAGAGGCGCAAGGGCATCCCATGGACGG
ATCACGAGGTTAACAATGGGGGATCGTCTCATCAAGC
                            ATCACCAGCGTCACCGCCGGCGATCAGGTCGCCGCGC
                                                                            AGTACTTCATCCGCCTCAACTCCATGAACCGCGACCGCCGCCGCCGCCCAGCATCCACGAC-
                                                                                                                  GCATTTCAAGGAACTTTGTGATATCGAGAACTCCGACGCAGGTGGCTAGCCATGCACAAA
                                                                                                                                                                            AAGAAGAGCATAGGTTATTTCTACTTGGTTTAGACAAGTTTGGGAAAGGAGATTGGAGAA
                                                                                                                                                                                                      AGGAAGAGCACAGGCTGTTCTTGCTGGGGGCTGGACAAGTTCGGCAAGGGGGACTGGCGGA
                                                                                                                                                                                                                                    ATGGAGGGAAACAGAGTTCGAGGTCCGACCAAGAAAGAAGGAAAGGAATCCCATGGACTG
                                                        AGTATTTTATACGCTTAAATTCGATGAATAGAGACCGGCGGCGGTCCAGCATCCACGACN
                                                                                                                                                                                                                                                                                              Conservative
                                                                                                                                                                                                                                                                                                       9.8%;
                                                                                                                                                                                                                                                                                            0;
                                                                                                                                                                                                                                                                                           Score 130.6; DB 12; Length 412; Pred. No. 4.9e-12; O; Mismatches 84; Indels 1;
                            671
 401
                                                                                                                                                                                                                                                                                            1;
                                                                                                                                                                                                                                                                                              Gaps
                                                                                      634
                                                                                                                                               575
                                                                                                                                                                                                                                    184
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                                                         364
                                                                                                                   304
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RESULT 5
ADC46626
ID ADC4
XX ADC4
AC ADC4
XX Thal
DF Thal
XX Thal
XX Thal
XX Thal
XX Thal
XX Tran
XX dise
XX dise
XX dise
XX Arab
XX US20
XX US20
XX TS-M
PP 15-M
XX US-N
PF 01-N
                                                                                                                                          18-DEC-2003 (first entry)
                                                                                                                                                              ADC46636;
                                                                                                                                                                                ADC46636 standard; DNA; 1432
                                                                                                                                                                                 В₽
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Thalecress transcription factor-like DNA G1362

disease resistance; plant. Thalecress; transcription factor-like protein; ds; seed trait; transgenic; gene; plant size; stress tolerance; yield; gene; plant size; stress tolerance;

Arabidopsis thaliana

15-MAY-2003.

01-NOV-2002; 2002US-00286264

The invention relates to a substantially purified nucleic acid molecule

23-MAR-1999;

99US-0125814P.

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5
                                                                                                                                                                                                               The invention relates to a transgenic plant having recombinant CC polynucleotide (II) encoding polypeptide comprising at least 6 consecutive amino acids of a sequence chosen from the protein sequence CC consecutive amino acids of a sequence chosen from the protein sequence CC encombinant polynucleotide alters a trait of the seed transgenic plant CC when compared with same trait of another plant lacking recombinant CC when compared with same trait of another plant lacking recombinant CC included are altering (MM) a trait associated with seed (comprising: CC transforming a plant with (II); selecting the transformed plants; and CC identifying a trait associated having altered trait), altering (M2) the expression levels of at least one gene of a plant (involving CC transforming the plant with (II) and selecting the transformed plant), CC altering (M3) a trait associated with a plant's seed (comprising a nucleotide sequence comprising least 18 consecutive nucleotide comprising a consecutive nucleotide comprising a nucleotide appearing the database sequence with a polypucleotide or a sequence, comparing the database sequence with a polypeptide or a complication of the plant) and altering a plant's trait (involving a database sequence in the plant) and altering a plant's trait (involving a database sequence in the plant) and altering a plant's trait (involving providing a test polynucleotide detailed above, selecting a database sequence (comprising the test polynucleotide with a polypeptide or a plant's trait (involving providing a test polynucleotide detailed above, selecting a trait of the polynucleotide detailed above at low stringency and transforming the sequence sequence comprise the comprise trait. The method (M3) is useful for altering a plant's trait (involving a protein) and intering a plant's trait of the present sequence sequence and trait altering a plant's trait is such as seed or plant size, stress tolerance, yield or disease contents, seed trait altering a protein of the invention.
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                                                                                                                                                                           Matches
                                                                                                                      Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Novel transgenic plant having recombinant polynucleotide encoding polypeptide that alters trait of transgenic plant when compared w trait of another plant lacking recombinant polynucleotide.
                                                                                                                                                                         Sequence 1432 BP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Disclosure; SEQ ID NO 35; 165pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 2003-765498/72.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Heard
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Keddie
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (HEAR/)
                                                                                                                                                                                                           protein/seed
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (RIEC/)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              22-MAR-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (PINE
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YU G.
ADAM L.
BROUN P.
REUBER L.
PILGRIM M.
SAMAHA R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ZHANG J.
JIANG C.
PINEDA O.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ADC46637.
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RATCLIFFE O.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            KEDDIE
 TTCTTGCTGGGGCTGGACAAGTTCGGCAAGGGGGGACTGGCGGAGCATCTCGCGCAACTTC
                                                             Yu G,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Riechmann JL,
Yu G, Adam L,
                                                                                                      Conservative
                                                                                                                                                                                                         trait altering protein of the invention.
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                                                                                                                                                                           426
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                                                                                                                   9.7%;
70.3%;
                                                                                                                                                                         A; 269 C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Ratcliffe O, Zha
Broun P, Reuber
                                                                                                      0
                                                                                                                      Score 129.2;
Pred. No. 8e
                                                                                                      Mismatches
                                                                                                                                                                         351 G;
                                                                                                                      8e-12;
                                                                                                                                                                         386 T; 0 U;
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ber L, Pilgrim M,
                                                                                                                                       DB 10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          plant when compared with same
                                                                                                      Indels
                                                                                                                                       Length 1432;
                                                                                                                                                                           0 Other;
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RESULT 6
ADD55829
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The invention relates to a recombinant polynucleotide that alters a plant's environmental stress tolerance when compared with the same trained another plant lacking the recombinant polynucleotide. Also included are a transgenic plant comprising the novel recombinant polynucleotide having a sequence that encodes a polypeptide comprising at least 6
                                                                                             New recombinant polynucleotide for altering the reeexpression of plants to modify the plant's traits,
                                                                                                                                                                       Samaha
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Thalecress; environmental stress; ss; gene; plant; viral infection; fungal infection; microbial infection; herbicide resistance; heat; heavy metal; low light; drought; osmotic stress; salt concentration
                                                                                     plant's environmental stress tolerance.
                                                                                                                                                                                                                                                           (RIEC/)
                                                                                                                                                                                                                                                                                                                                             23-MAR-1999;
22-MAR-2000;
                                                                                                                                                                                                                                                                                                                                                                            22-OCT-2002; 2002US-00278536
                                                                                                                                                                                                                                                                                                                                                                                                                      US2003131386-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                       Arabidopsis thaliana.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Thalecress environmental stress-related cDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       15-JAN-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADD55829
                                                                                                                                                                                                                                                                                                                                                                                                 10-JUL-2003
                                                                                                                                                                                                                             (PILG/
                                                                                                                                                                                                                                      (RATC/)
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                                                                                                                                                                                                                                                                                          (PINE/)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            760
                                                                                                                                                             R, Heard J, Jiang (
Keddie J, Ratcliffe
                                                                                                                                                                                                                          KEDDIE J.
RATCLIFFE
PILGRIM M.
                                                                                                                                                                                                                                                                               HEARD J.
JIANG C.
PINEDA O.
REUBER L.
                                                                                                                              ADD55830.
                                                                                                                                                                                            BROUN
ZHANG
                                                                                                                                                                                                                 ADAM L.
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2
                                                                                                                                                                                                                                                                     RIECHMANN
                                                                                                                                                                                                                                                                                                                        SAMAHA R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                standard; cDNA; 1432
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GCAGAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GGCGAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AATTCAATGAACAAAGACAGAAGGCGATCAAGCATTCACGACATCACTAGTGTTGGCAAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AACTCCATGAACCGCGACCGCCGCCGCTCCAGCATCCACGACATCACCAGCGTCACCGCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GTAGTAACAAGAACACCGACCCAAGTTGCGAGCCATGCTCAAAAGTATTTCATTCGTCTA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GTCATCTCGCGGACGCCAACGCAGGTGGCGAGCCACGCGCAGAAGTACTTCATCCGCCTC
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                                                                 SEQ ID
                                                                                                                                                                                                                                                                                                                                              2000US-00532591
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                                                                 187;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       entry)
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                                                                                                                                                          , o,
                                                                                                                                                            Pineda O,
Pilgrim
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                         stress; salt concentration;
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, Adam
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                                                                                              regulation of gene
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                                                                                                                                                             Riechmann
Broun P,
                                                                                                                                                              JL;
Zhang
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ADI61458

ADI61458

ADI61458

ADI61458

AC ADI6

XX ADI6

XX ADI6

XX CON/

XX Plar

XX Plar

XX US2

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XX US2

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XX II-I

XX II-I

PR 22-I

PR 22-I

PR 11-I

PR 11-I

PR 22-I

PR 22-I

PR 22-I

PR 22-I

PR 21-I

PR 
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Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Matches 173;
                                                                                                                                                   18-FEB-1999;
22-FEB-1999;
11-MAR-1999;
15-APR-1999;
20-MAY-1999;
15-JUL-1999;
22-OCT-1999;
01-NOV-1999;
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                        (KEDD/)
(FROM/)
(HEAR/)
                                                                                                                                                                                                                                                                                                                                                                                        22-NOV-2002;
                                                                                                                                                                                                                                                                                                                                                                                                                                           11-DEC-2003.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Arabidopsis thaliana.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Plant; transcription factor; TF; plant trait; gene; ss
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              cDNA encoding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    22-APR-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ADI61458;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ADI61458 standard; cDNA; 1432
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 1432 BP; 426 A; 269 C; 351 G; 386 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    820
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        413
) FROMM M.
) HEARD J.
) RIECHMANN J L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Similarity
                                                                          KEDDIE J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TCCAAGGCGGAGCAGGAGAGGCGCAAGGGCATCCCATGGACGGAGGAAGAGCACAGGCTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GCAGAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GGCGAT 658
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AATTCAATGAACAAAGACAGAAGGCGATCAAGCATTCACGACATCACTAGTGTTGGCAAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AACTCCATGAACCGCGACCGCCGCCGCTCCAGCATCCACGACATCACCAGCGTCACCGCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GTAGTAACAAGAACACCGACCCAAGTTGCGAGCCATGCTCAAAAGTATTTCATTCGTCTA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GTCATCTCGCGGACGCCAACGCAGGTGGCGAGAGCCACGCGCAGAAGTACTTCATCCGCCTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TTTCTTCTTGGTTTGGATAAGTACGGGAAAGGTGATTGGCGTAGCATTTCTCGCAACTTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TTCTTGCTGGGGCTGGACAAGTTCGGCAAGGGGGGACTGGCGGAGCATCTCGCGCAACTTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TCAAAGTCCGATCAAGAACGACGAAAGGGTATCGCGTGGACAGAAGATGAGCACAGGTTA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
                                                                                                                                                                                                                                                                                                                                                                                      2002US-00302267
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (first entry)
                                                                                                                                2000US
                                                                                                                                                99US-0120880P.
99US-0121037P.
99US-0124278P.
99US-0129450P.
99US-0135134P.
99US-0161143P.
99US-0162656P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A. thaliana novel transcription factor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    825
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 129.2;
Pred. No. 8e-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ВP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     8e-12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DB 10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     73;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 1432;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (TF)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0,
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RESULT 8

ADO02450;

ADO02450 standard; cDNA; 1432

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                                                                                                                                                                                                                                                                                                                                                                                       The present invention relates to the isolation of novel plant (arabidopsis thallana) polynucleotide sequences that encode transcription (factors (TFs), and the polypeptide sequences for the TFs. The polynucleotide sequences for the TFs. The complete sequences are useful in screening for a transcription of factor that modifies a plant trait. Also disclosed is an expression comparising a TF polynucleotide sequence, a host cell comprising the expression vector, a transgenic plant comprising or ectopically compressing an isolated TF polynucleotide sequence, a method for screening for a molecule that modifies a plant trait, a method for producing a complete sequence thomologous to a TF polynucleotide or polynucleotide sequence, and a method for screening for a modifies a plant trait. The present sequence conducted a novel A. thaliana TF of the invention. Note: The sequence data for this patent did not form part of the printed specification. The complete sequence data for this patent as obtained in electronic format contractly from the HERPON who site at senders unstained in electronic format contractly from the HERPON who site at senders unstained in electronic format contractly from the HERPON who site at senders unstained in electronic format contractly from the HERPON who site at senders unstained in electronic format contents.
                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local :
                                                                                                                                                                                                                                                                                                                          Matches
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Pineda O,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (BROU/)
(PINE/)
(REUB/)
(ZHAN/)
(YUGG/)
                                                                                                                                                                                                                                                                                                                                                                                       Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                P-PSDB; ADI61459.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               modifies a plant trait
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Creelman
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (JIAN/)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (CREE/)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (SAMA/)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                polynucleotide, useful
                                                                                                                                                                                                                                                           580
820
                                                             760
                                                                                             593
                                                                                                                             700
                                                                                                                                                           533
                                                                                                                                                                                           640
                                                                                                                                                                                                                         473
                                                                                                                                                                                                                                                                                         413
                                                                                                                                                                                                                                                                                                                         173;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             BROUN P.
PINEDA O.
REUBER L.
ZHANG J.
YU G.
JIANG C.
SAMAHA R.
PILGRIM M.
                                                                                                                                                                                                                                                                                                                                        Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CREELMAN R.
                                                                                                                                                                                                                                                                                                                                                                                                                      from
                                                                                                                                                GTCATCTCGCGGACGCCAACGCAGGTGGCGAGGCCACGCGCGCAGAAGTACTTCATCCGCCTC
                                                                                                                                                                                                              TICTIGCTGGGGCTGGACAAGTTCGGCAAGGGGGACTGGCGGAGCATCTCGCGCAACTTC
                                                                                                                                                                                                                                                           TCAAAGTCCGATCAAGAACGACGAAAGGGTATCGCGTGGACAGAAGATGAGCACAGGTTA
                                                                                                                                                                                                                                                                               TCCAAGGCGGAGCAGGAGAGGCGCAAGGGCATCCCATGGACGGAGGAGGAAGAGCACAGGCTG
                                                                                                                                                                                                                                                                                                                                                                                       1432 BP; 426 A; 269 C; 351 G; 386 T; 0 U;
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 GCAGAT
                                 GGCGAT
                                                                                             AACTCCATGAACCGCGACCGCCGCCGCCCCAGCATCCACCATCACCAGCGTCACCGCC
                                                                                                                             GTAGTAACAAGAACACCGACCCAAGTTGCGAGCCATGCTCAAAAGTATTTCATTCGTCTA
                                                                                                                                                                                             TTTCTTCTTGGTTTGGATAAGTACGGGAAAGGTGATTGGCGTAGCATTTCTCGCAACTTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQ ID NO 157; 16pp;
                                                             AATTCAATGAACAAAGACAGAAGGCGATCAAGCATTCACGACATCACTAGTGTTGGCAAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Reuber
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                                                                                                                                                                                                                                                                                                                         Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                      the USPTO web site at segdata.uspto.gov.
                              658
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                                                                                                                                                                                                                                                                                                                                      9.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Heard J,
Zhang J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                'n
                                                                                                                                                                                                                                                                                                                       0;
                                                                                                                                                                                                                                                                                                                       Score 129.2; DB
Pred. No. 8e-12;
D; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                screening
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Riechmann JL, A
Yu G, Jiang C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 for
                                                                                                                                                                                                                                                                                                                                                       DB 12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 a transcription
                                                                                                                                                                                                                                                                                                                     73;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Adam L, Bro
C, Samaha R,
                                                                                                                                                                                                                                                                                                                         Indels
                                                                                                                                                                                                                                                                                                                                                       Length 1432;
                                                                                                                                                                                                                                                                                                                                                                                       0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Broun P;
                                                                                                                                                                                                                                                                                                                       0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   factor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Pilgrim
                                                                                                                                                                                                                                                                                                                       Gaps
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                                                             819
                                                                                               652
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                                                                                                                                                                                                                             532
                                                                                                                                                                                                                                                           639
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30-JAN-2002;
14-JUN-2002;
09-AUG-2002;
                                                                                                                                                                                                                                                                                                                                                                                            22-MAR-2000;
22-MAR-2000;
22-MAR-2000;
22-MAR-2000;
22-MAR-2000;
06-APR-2000;
16-NOV-2000;
17-MAR-2001;
17-MAR-2001;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           trichome development; seed development; premature senescence;
delayed senescence; lethality; necrosis; plant size; leaf morphology;
seed morphology; secondary metabolism; light response; shade avoidance
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Thalecress; transcription factor; ss; gene; plant; transgenic; abiotic stress; cold tolerance; heat tolerance; cought; osmotic phosphate limitation; photassium limitation; nitrogen limitation; phormone sensitivity; disease resistance; sugar sensing; seed gern flowering; inflorescence architectural change; meristem cell differentiation; phyllotaxy; apical dominance; meristem cell differentiation; phyllotaxy; apical dominance;
                 New transgenic plant, use improved characteristics
                                                 WPI; 2004-225755/21.
P-PSDB; ADO02451.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              10-APR-2003; 2003US-00412699
                                                                                        Pilgrim
                                                                                                                                         (DUBE/)
(RATC/)
(KUMI/)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       21-JAN-2000;
17-FEB-2000;
                                                                                                                                                                                (SAMA/)
                                                                                                                                                                                                    (YUGG,
                                                                                                                                                                                                                                  (REUB,
                                                                                                                                                                        CREE/)
                                                                           TJ,
m ML,
m BK;
                                                                                                                                                                                                                                                                                                                          -2002;
-2003;
                                                                                                                              JIANG C.
SAMAHA R S.
PILIGRIM M L.
CREELMAN R A.
DUBELL A N.
RATCLIFFE O.
KUMIMOTO R.
SHERMAN B K.
                                                                                                                                                                                                                                                                       FROMM M E.
HEARD J E.
RIECHMANN J L.
                                                                                                                                                                                                              PINEDA O.
REUBER T L.
KEDDIE J S.
YU G.
                                                                                                                                                                                                                                                   ADAM L J.
BROUN P E.
                                                                                       Fromm ME, H
Reuber TL,
fL, Creelman
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              transcription
                                                                                                                                                                                                                                                                                                                                                                ; 2000US-00713994.
; 2001US-00819142.
; 2001US-00837444.
; 2002US-00958131.
; 2002US-00171468.
; 2002US-00171468.
                                                                                                                                                                                                                                                                                                                                                                                                                                     2000US-00533392.
2000US-00533392.
2000US-00533648.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2000US-00532591.
2000US-00533029.
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2000US-00506720.
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                                                                                                                                                                                                                                                                                                                                                                                                                            2000WO-US009448.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (first entry)
                                                                                                                                                                                                                                                                                    434
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           9908-00394519
                                                                                       Heard JE, Riechmann JL, Ao
, Keddie JS, Yu G, Jiang O
nn RA, Dubell AN, Ratcliffe
                            useful in developing
                   or traits.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               factor cDNA #432
                            phenotypes with altered
                                                                                                            Adam
                                                                                     0.0
                                                                                                            Ę
                                                                                                   Samaha
                                                                                         Kumimoto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 osmotic stress;
                                                                                                           Broun PE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              germination;
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SEQ

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863; 213pp; English

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AATTCAATGAACAAAGACAGAAGGCGATCAAGCATTCACGACATCACTAGTGTTGGCAAC AACTCCATGAACCGCGACCGCCGCCGCCTCCAGCATCCACGACATCACCAGCGTCACCGCC S 밁 Ś

GTCATCTCGCGGACGCCAACGCAGGTGGCGAGCCACGCGCAGAAGTACTTCATCCGCCTC TTTCTTCTTGGTTTGGATAAGTACGGGAAAGGTGATTGGCGTAGCATTTCTCGCAACTTT TTCTTGCTGGGGCTGGACAAGTTCGGCAAGGGGACTGGCGGAGCATCTCGCGCAACTTC TCAAAGTCCGATCAAGAACGACGAAAGGGTATCGCGTGGACAGAAGATGAGCACAGGTTA TCCAAGGCGGAGCAGGAGAGGCGCAAGGGCATCCCATGGACGGAGGAAGAGCACAGGCTG

699

639

GTAGTAACAAGAACACCGACCCAAGTTGCGAGCCATGCTCAAAAGTATTTCATTCGTCTA

652

759

819

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Matches Query Match Best Local

173;

Conservative

0,

Pred. No. 8e-); Mismatches Score 129.2;

DB 12;

Length 1432;

0,

Gaps

Similarity

70.3%; 9.7%;

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Coassette, producing a modified plant having a modified trait, identifying a factor that is modulated by or interacts with a polypeptide encoded by the polypucleotide sequence and identifying at least one downstream copynucleotide sequence and identifying at least one downstream copynucleotide sequence and identifying at least one downstream copynucleotide sequence that is subject to a regulatory effect of any of the polypucleotide described above. The character is useful for producing a plant that has an altered traits e.g. an enhanced tolerance to abiotic stress (increased tolerance to heat, tolerance to observe the conditions, freezing tolerance to common to cold conditions, freezing tolerance to the conditions, tolerance to potassium the cold indication, decreased sensitivity to mitrogen limitation, altered susceptibility to producing a latered susceptibility to cold the conditions, tolerance to potassium and the cold conditions to the cold, an altered susceptibility to science to ensitivity to abscisic acid, an altered susceptibility to science thinks, altered susceptibility to science thinks, altered susceptibility to science thinks, altered susceptibility to science architectural change, altered susceptibility to science architectural change, actange in set mbifurcations, alack of a shoot meristem, reduced meristem cell captions of flowering, altered specific crichome development, altered stem morphology, increased root thairs, altered stem morphology, increased root fairs, altered stem morphology, increased cold aftered traition, increased plant size, a change in leaf morphology, increased to root of content, an alteration of leaf glucosinolate content, change in seed of susceptibility acid content, decreased leaf anthocyanins, an alteration of leaf flucosinolate content, change in seed of scoulate in protein content, decrease in seed fatty acid content, increase in seed fatty acid content, decrease in seed fatty acid content, decrease in seed fatty acid content, decrease in seed fatty acid content, sec
     The invention relates to a transgenic plant comprises a recombinant polynucleotide having a polynucleotide sequence or its complementary sequence comprising a sequence encoding a polypeptide, that initiates transcription (i.e. a transcription factor) from Arabidopsis, Soybean, Rice, Rape or Corn, comprising any of the sequences appearing as ADO01588-AD003527 or AD003530-AD003559. Also included are using a transgenic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              plant to grow a progeny plant, an expression cassette (comprising a constitutive, inducible or tissue-specific promoter and a recombinant polynucleotide described above), a host cell comprising the expression
Sequence 1432 BP; 426 A; 269 C; 351 G; 386 T; 0 U; 0 Other:
                                                   ot anthocyanins, increase in plant anthocyanins, and alteration response or shade avoidance. The present sequence encodes a cress transcription factor of the invention.
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밁 8

GCAGAT 825

.53 820

GGCGAT 658

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                                                                                                                                                                                               The invention relates to a novel isolated polynucleotide comprising a CC first nucleotide encoding a polypeptide of 217, 120, or 268 amino acids that has 85%, 95%, or 96% identity based on the clustal method of CC alignment when compared to a polypeptide selected from Myb polypeptides sequences of 128, 258, or 268 amino acids fully defined in the Specification, or a second nucleotide sequence comprising the complement CC specification, or a second nucleotide for sequence comprising the complement CC of the first nucleotide. The isolated polynucleotide is useful for obtaining a nucleic acid fragment encoding an Myb-related transcription factor polypeptide by using it to probe cDNA or genomic libraries. A CC factor polypeptide by using it to probe cDNA or genomic libraries. A CC funcleic acid fragment obtained using the isolated polynucleotide is useful to isolate cDNAs and genes encoding homologous proteins from the constant or other plant species. The nucleic acid fragment is also useful to create transgenic plants in which the Myb-like protein is present at higher or lower levels than normal or in cell types. This polynucleotide is sequence represents the DNA of an Myb-related transcription factor of the
                                                                                           Query Match
Best Local Similarity
Matches 200; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Cahoon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Glycine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ABT08115 standard; DNA; 1119 BP
                                                                                                                                                      Sequence 1119
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 2; Page 18-19; 51pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Novel isolated polynucleotide useful for obtaining a nucleic acid fragment encoding a Myb-related transcription factor polypeptide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (RAFA/)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (LIUZ/)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     20-NOV-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                30-MAY-2008
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US2002066120-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Myb; Myb-related
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Myb-related transcription factor DNA SEQ ID No 9.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           21-NOV-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ABT08115;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    19-NOV-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (CAHO/) CAHOON R E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2002-556780/59
 389
                              249
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WENG Z.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RAFALSKI J A.
SHI J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ODELL J T.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ABJ10411.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LIU Z.
 GGGTACGACGGCGCAAGAGCTGCTCCAAGGCGGAGCAGGAGAGGCGCAAGGGCATCCCA
                                GACGCCACCACCACCAACAACAACAAGACGCCGTCGCCGCCGGCTACGCCTCCGCCGAC
                                                        Liu Z,
                                                                                             Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (first entry)
                                                                                                                                                      BP;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            transcription factor; plant; transgenic plant; gene;
                                                                                                                                                      301 A; 305 C; 256 G; 254 T; 0 U; 3 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0de11
                                                                                                      9.5%;
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                                                                                             0
                                                                                           Score 126.8; DB 6;
Pred. No. 1.9e-11;
0; Mismatches 124;
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                                                                                                                          Length 1119;
                                                                                             Indels
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                                                                                             <u>.</u>
                                                                                           Gaps
   448
                                                              388
                                308
                                                                                             0
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Query Match Best Local S Matches 200

Local Similarity 61. les 200; Conservative

9.5%; 61.7%;

0;

Score 126.8; DB 12; Length 1119; Pred. No. 1.9e-11; 0; Mismatches 124; Indels 0;

Gaps

0

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RESULT 10
RDH50105
RXX ADH500
XX ADH500
XX ADH50
XX ADH50
XX ADH50
XX ADH50
XX ADH50
XX APS-E
XX MYD-E
XX Glyci
XX Glyci
XX I12-DE
XX I2-DE
XX I2-DE
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PR 19-NC
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PR 19-NC
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                                           The invention comprises the amino acid and coding sequences of Mybrelated transcription factors - these proteins are involved in transcriptional regulation in plants. The DNA and protein sequences of the invention may be used to facilitate studies to better understand gene regulation in plants and provide genetic tools to enhance or otherwise alter the expression of genes controlled by Myb-related transcription factors. The present DNA sequence encodes an Myb-related transcription
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Myb-related transcription factor; transcriptional regulation; gene regulation; soybean; gene; ds.
 Sequence
                                                                                                                                                                          Claim 2; SEQ ID NO 9; 53pp; English
                                                                                                                                                                                                       expression.
                                                                                                                                                                                                                       A new isolated plant nucleic acid fragments encoding transcription factor in plants and seeds, are useful
                                                                                                                                                                                                                                                                       WPI; 2004-059062/06.
P-PSDB; ADH50106.
                                                                                                                                                                                                                                                                                                                        Cahoon RE,
                                                                                                                                                                                                                                                                                                                                                                                                      20-NOV-1998;
19-NOV-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                    05-DEC-2001; 2001US-00008118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US2002187539-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Glycine max.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Soybean Myb-related transcription factor coding sequence #3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              25-MAR-2004 (first entry)
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                                 factors. The 
factor of the
                                                                                                                                                                                                                                                                                                                                                    (CAHO/) CAHOON R E. (WENG/) WENG Z.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     12-DEC-2002
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 1119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GCTCAGAAGTACTTTCTCCGACGAAGCAACCTCAATCGCCGTCGCCGTAGATCCAGCCTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TGGCGGAGCATCTCGCGAACTTCGTCATCTCGCGGACGCCAACGCAGGTGGCGAGCCAC 568
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TGGACGGAGGAAGAGCACAGGCTGTTCTTGCTGGGGCTGGACAAGTTCGGCAAGGGGGAC 508
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TGGÁCGGAGGAAGAACACAAGTTGTTTTTGGTTGGATTGCACAAAGTANGGAAAGGTGAT 428
                                                                                                                                                                                                                                                                                                                      Weng
BP;
                                 invention.
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99US-00443704
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 301
A; 305
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 256 G;
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 254 T;
 0 U;
   3 Other;
                                                                                                                                                                                                                         a Myb-related to control gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 plant;
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RESULT 11
ADQ03867
ID ADQ03
AC ADQ03
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  24-NOV-1997
09-DEC 1997
13-JAN 1998
10-FEB-1998
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12-FEB-1998
12-FEB-1998
19-FEB-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               maize; soybean; Arabidopsis thaliana; transcription factor; homeobox; HLH; leucine zipper; zinc finger; transformed plant; plant; metabolic pathway; mutation detection; polymorphism; plant trait; genome mapping; gene identification; gene analysis; plant breeding; transgenic; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         06-AUG-2001;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TGGAGAGGAATCTCCAAAAACTACGTCAAAACGCGAACGCCAACGCAGGTTGCGAGCCAT
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98US-0071479P

98US-0074281P

98US-0074281P

98US-0074565P

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98US-0074769P

98US-0075461P

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98US-0075461P

98US-0075461P

98US-0075461P

98US-0077231P

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98US-0077231P

98US-0078368P

98US-0083067P

98US-0083067P
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29 APR-1998
13-MAY 1998
13-MAY 1998
15-MAY 1998
21-MAY 1998
21-MAY 1998
21-MAY 1998
21-MAY 1998
21-MAY 1998
21-MAY 1998
118-JUN 1998
119-SEP 1998
118-JUN 1998
11
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(HECK/)
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29-APR-1998;
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98US-0083388P.
98US-0085232P.
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98US-008618P.
98US-0089807P.
98US-0089811P.
98US-0089812P.
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98US-0089813P.
98US-0089813P.
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98US-009967P.
98US-009967P.
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98US-0010674P.
98US-0101347P.
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98US-01013224P.
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TW, Heck GR, Liu Ç

2004-468202/44.

New substantially purified nucleic acid molecule that encodes a maize, soybean or Arabidopsis thaliana transcription factor or its fragment, useful for genome mapping, gene identification and analysis or plant

Claim *ې* SEQ ü ŏ 713; 140pp; English.

The invention describes a substantially purified nucleic acid molecuthat encodes a maize, soybean or Arabidopsis thaliana transcription factor or its fragment, where the maize or soybean transcription fac is homeobox, HLH, leucine zipper, zinc finger, or other transcriptic factor. Also described are: a substantially purified maize or soybean transcription ize or soybean molecule factor

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Best Local S
Matches 182
24-NOV-1997;
09-DEC-1997;
13-JAN-1998;
10-FEB-1998;
10-FEB-1998;
10-FEB-1998;
                                                                                                                                                                                                 maize; soybean; Arabidopsis thaliana; transcription factor; homeobox; HLH; leucine zipper; zinc finger; transformed plant; plant; metabolic pathway; mutation detection; polymorphism; plant trait; genome mapping; gene identification; gene analysis; plant breeding; transgenic; ds.
                                                                                            06-AUG-2001;
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                                                                                                                                                                                                                                                                                                                                                                   standard; DNA; 386
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ilarity 74.6%;
Conservative
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97US-0067000P.
97US-0069472P.
98US-0071479P.
98US-0074201P.
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98US-0074281P.
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Pred. No. 7.5e-
0; Mismatches
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18-JUN-1998
11-SEP-1998
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16-SEP-1998
17-SEP-1998
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11-SEP-1998
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29-APR-1998;
13-MAY-1998;
13-MAY-1998;
13-MAY-1998;
15-MAY-1998;
21-MAY-1998;
21-MAY-1998;
21-MAY-1998;
21-MAY-1998;
21-MAY-1998;
21-MAY-1998;
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07-APR-1998;
27-APR-1998;
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19-FEB-1998;
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12-FEB-1998;
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09-MAR-1998
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09-MAR-1998;
  (CONN/)
 CONNER
HECK G
                                                                                98US-0075462P

98US-0075463P

98US-0077231P

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98US-0077231P

98US-008338P

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98US-0085223P

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RESULT 13
ADQ03772
ID ADQ03
XX ADQ03
XX ADQ03
XX O9-SE
XX Maize
XX Maize
XX Maize
KW HLH;
KW Metab
KW Genom
KW Trans
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Best Local
                       maize; soybean; Arabidopsis thaliana; transcription factor; homeobox;
HLH; leucine zipper; zinc finger; transformed plant; plant;
metabolic pathway; mutation detection; polymorphism; plant trait;
genome mapping; gene identification; gene analysis; plant breeding;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          New substantially purified nucleic acid molecule that encodes a maize, soybean or Arabidopsis thaliana transcription factor or its fragment, useful for genome mapping, gene identification and analysis or plant
                                                                                        Maize transcription
                                                                                                                 09-SEP-2004
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 386 BP;
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              transgenic;
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77.2%;
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                                                                                       seqid 618.
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Pred. No. 2.3e-10;
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   16-SEP-1998
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22-SEP-1998
22-SEP-1998
22-SEP-1998
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22-SEP-1998
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09-SEP-1998;
09-SEP-1998;
09-SEP-1998;
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18-JUN-1998;
30-JUN-1998;
30-JUN-1998;
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21-MAY-1998;
21-MAY-1998;
21-MAY-1998;
16-JUN-1998;
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13-MAY-1998;
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                                                                                                                                                                                                                                                                                                                                 CC is homeobox. Hill, leucine zipper, zinc finger, or other transcription CC factor. Also described are: a substantially purified maize or soybean CC transcription factor or its fragment defined above; a substantially CC purified antibody or its fragment which is capable of specifically CC binding to the transcription factor or its fragment above; a transformed CC plant; a method for determining a level or pattern in a plant cell of a CC determining a mutation in a plant method ic pathway; a method of CC determining a nutation in a plant; a method of producing a plant CC containing an overexpressed protein ore reduced levels of plant CC transcription factor; a method of determining an association between a polymorphism and a plant trait; and a method of isolating a nucleic acid CC that encodes a plant transcription factor or its fragment. The nucleic CC acid molecules, proteins and their fragments are useful for genome CC constructs for use in plant gene expression and transgenic plants. The CC constructs for use in plant gene expression and transgenic plants. The CC represents a maize transcription factor polynucleotide.
                                                                                                                                                                                                                                           Best Local Sim Matches 145;
                                                                                                                                                                                                                                                                          Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              08-DEC-1998;
11-DEC-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          13-OCT-1998;
13-OCT-1998;
13-OCT-1998;
13-OCT-1998;
18-NOV-1998;
                                                                                                                                                                                                                                                                                                          Sequence 315 BP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The invention describes a substantially purified nucleic acid molecuthat encodes a maize, soybean or Arabidopsis thaliana transcription factor or its fragment, where the maize or soybean transcription fa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                breeding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New substantially purified nucleic acid molecule that encodes a maize, soybean or Arabidopsis thaliana transcription factor or its fragment, useful for genome mapping, gene identification and analysis or plant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conner TW,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (CONN/)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 22-DEC-1998;
12-JAN-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             19-NOV-1998;
24-NOV-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2004-468202/44
309
                           641
                                                         249
                                                                                       581
                                                                                                                     189
                                                                                                                                                  521
                                                                                                                                                                                                               461
                                                                                                                                                                                  129
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CONNER
HECK G
LIU J.
                                                                                                                                                                                                                                                             Similarity
                                                                                                                                     TCGCGCAACTTCGTCATCTCGCGGACGCCAACGCAGGTGGCGAGCCACGCGCAGAAGTAC
                                                                                                                                                                                                               GAGCACAGGCTGTTCTTGCTGGGGGCTGGACAAGTTCGGCAAGGGGGACTGGCGGAGCATC
ACGGTGA 315
                           AGCGTCA 647
                                                                              TTCATCCGCCTCAACTCCATGAACCGCGGACCGCCGCCGCCTCCAGCATCACGACATCACC
                                                                                                                                                                                  GGGGCCAGGCTGTTCCTCTTAGGCCTGAAGAAATACGGCAAGGGGGACTGGAGGAACATA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQ ID NO
                                                            TTCATCAGGCTCAACTCCGGCGGCAAGGACAAGAGGAGGTCCAGCATCCACGACATCACC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Heck GR,
                                                                                                                                                                                                                                             Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               98US-0104124P.
98US-0104127P.
98US-0104127P.
98US-0104128P.
98US-0108996P.
98US-010199129.
98US-00199129.
98US-001199129.
98US-00111981P.
98US-0113224P.
99US-00229413.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ⊅ H
€
                                                                                                                                                                                                                                                                                                          85
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               618; 140pp; English.
                                                                                                                                                                                                                                                                                                        A; 81 C; 86 G; 63 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                           9.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Liu
                                                                                                                                                                                                                                           Score 119.8; DB Pred. No. 2.6e-10; Mismatches
                                                                                                                                                                                                                                             ..
                                                                                                                                                                                                                                                             .6e-10;
                                                                                                                                                                                                                                                                          DB 12;
                                                                                                                                                                                                                                               Indels
                                                                                                                                                                                                                                                                          Length
                                                                                                                                                                                                                                                                           315;
                                                                                                                                                                                                                                             0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    molecule
                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       factor
                                                                                       640
                                                                                                                                                    580
                                                                                                                                                                                  188
                                                                                                                                                                                                                520
                                                                                                                     248
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RESULT 14 ADQ03861

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Maize transcription factor
                        09-SEP-2004
                                                                       ADQ03861 standard;
                        (first entry)
                                                                       DNA;
                                                                       144
segid 707.
                                                                       ₽P
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maize; soybean; Arabidopsis thaliana; transcription factor; homeobox; HLH; leucine zipper; zinc finger; transformed plant; plant; metabolic pathway; mutation detection; polymorphism; plant trait; genome mapping; gene identification; gene analysis; plant breeding; transgenic; ds.

19-FEB-1998;
09-MAR-1998;
09-MAR-1998;
09-MAR-1998;
18-MAR-1998;
27-APR-1998;
29-APR-1998;
29-APR-1998;
29-APR-1998;
13-MAY-1998;
13-MAY-1998;
13-MAY-1998;
15-MAY-1998;
21-MAY-1998;
21-MAY-1998; 06-AUG-2001; 19-FEB 12-FEB-1998 19-FEB-1998 10-FEB-1998 10-FEB-1998 2001US-00922293 98US-0075462P 98US-0075463P 98US-007723P 98US-007723P 98US-0077231P 98US-0077231P 98US-0080844P 98US-0083386P 98US-0083388P 98US-0085222P 98US-0085223P 98US-0085223P 98US-0085223P 98US-0086184P 98US-0086184P 98US-0086184P 98US-0086184P 98US-0086184P 98US-0086184P 98US-0089812P 98US-0089811P 98US-0089811P 98US-0089811P 98US-00991247P 98US-00991247P 98US-00991247P 98US-00991247P 98US-0099667P 98US-0099667P 97US-0067000P. 97US-0069472P. 98US-0071479P. - SUB 6 - SUB 98US--SU86 98US-0074280P 3-0074281P.
3-0074282P.
3-0074565P.
3-0074567P.
3-0074789P.
3-0075459P.

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                                                                                                                                                                                     The invention describes a substantially purified nucleic acid molecule CC that encodes a maize, soybean or Arabidopsis thaliana transcription factor or its fragment, where the maize or soybean transcription factor is homeobox, HLH, leucine zipper, zinc finger, or other transcription factor is homeobox, HCH, leucine zipper, zinc finger, or other transcription factor or its fragment defined above; a substantially purified antibody or its fragment which is capable of specifically comparing to the transcription factor or its fragment above; a transformed company is method for determining a level or pattern in a plant cell of a transcription factor in a plant metabolic pathway; a method of determining a mutation in a plant; a method of producing a plant containing an overexpressed protein ore reduced levels of plant transcription factor; a method of determining an association between a collymorphism and a plant transcription factor or its fragment. The nucleic cacid molecules, proteins and their fragments are useful for genome constructs for use in plant gene expression and transgenic plants. The nucleic acid molecules are in plant gene expression and transgenic plants. The nucleic acid molecules are useful as markers or probes. This sequence
                                                                                         Matches
                                                                                                   Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          21-SEP 1998;
21-SEP 1998;
22-SEP 1998;
22-SEP 1998;
22-SEP 1998;
22-SEP 1998;
23-SEP 1998;
13-OCT 1998;
13-OCT 1998;
13-OCT 1998;
13-OCT 1998;
13-OCT 1998;
13-OCT 1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    09-SEP-1998;
09-SEP-1998;
16-SEP-1998;
16-SEP-1998;
16-SEP-1998;
17-SEP-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New substantially purified nucleic acid molecule that encodes a maize, soybean or Arabidopsis thaliana transcription factor or its fragment, useful for genome mapping, gene identification and analysis or plant
                                                                                                                                                  Sequence 144 BP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 2; SEQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  OB-DEC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              24-NOV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      21-SEP-1998
                                                                                                                                                                               represents a
   488
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2004-468202/44
                                                                                         128;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TW, Heck GR,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CONNER
HECK G
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LIU J.
                                               GAGAGGCGCAAGGGCATCCCATGGACGGAGGAAGAGAGACAGGCTGTTCTTGCTGGGGCTG
GACAAGTTCGGCAAGGGGACTGGCGGAGCATCTCGCGCAACTTCGTCATCTCGCGGACG
                             GAGCGGCGCAAGGGCGTGCCGTGGACGGAAGAGGAGCACAGGTTGTTCTTGTTGGATCTG
                                                                                       Conservative
                                                                                                                                                                             maize transcription
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ID NO 707; 140pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           98US-0101131P
98US-0101132P
98US-0101343P
98US-0101344P
98US-0101544P
98US-0101547P
98US-0101707P
98US-0104124P
98US-0104124P
98US-0104127P
98US-0104128P
98US-0104128P
98US-0104128P
98US-0104128P
98US-0109918P
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                                                                                                                                                  27
                                                                                                  8.9%;
                                                                                                                                                A; 39 C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Liu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Ç
                                                                                      0;
                                                                                                                                                  54
                                                                                    Score 119; DB 12;
Pred. No. 3.6e-10;
D; Mismatches 15
                                                                                                                                                Ģ
                                                                                                                                                                             factor polynucleotide
                                                                                                                                                24 T;
                                                                                                                                                0 U; 0 Other;
                                                                                       15;
                                                                                                                 Length
                                                                                       Indels
                                                                                       0
547
                             61
                                                                                      0
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sequences

comprising inputting sequence information selected

from one

'n

sequences

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RESULT 15
ABK65275
ID ABK65275
AC ABK6
XX ABK6
XX ABK6
XX ABK6
XX ABK6
XX APA
DE Arah
XX Plar

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             망
                                    The invention relates to 1 of 232 isolated or recombinant polynucleotides encoding an Arabidopsis thaliana transcription factor, their variants, complements, fragments, or related polynucleotide with 31% to 95% sequence identity, where the plant possesses an altered trait as compared to a wild-type or reference plant, or the plant exhibits an altered phenotype as compared to a wild-type or reference plant, or the plant exhibits ectopic expression or altered expression of one or more genes associated with a plant trait as compared to a wild plant. Also included are a transgenic plant comprising the polynucleotides, a computer readable medium having stored sequence information, and identifying a homologue sequence from a database comprising a plurality of known plant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Plant; ss; gene; transcription factor; transgenic; agricultus, metabolic chemical; environmental stress; drought; microbial disease resistance; herbicide resistance; seed yield; fruit yield; growth rate; leaf senescence; flower senescence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 22-AUG-2000; 2000US-0227439P.
16-NOV-2000; 2000US-00713994.
18-APR-2001; 2001US-00837944.
                                                                                                                                                                                                                                                                                                                                                                                                                          An isolated or recombinant polynucleotide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Adam
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pilgrim
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (HEAR/)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (MEND-)
(PILG/)
(CREE/)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Arabidopsis thaliana.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Arabidopsis cDNA encoding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            02-JUL-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ABK65275;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ABK65275 standard; cDNA; 867
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (REUB/)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   22-AUG-2001;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (RATC/)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (ADAM/)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (KEDD/)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2002-292022/33.
DB; AAU93089.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   548
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CREELMAN R.
DUBELL A J.
HEARD J.
JIANG C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RATCLIFF O. REUBER J L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   M, Creelman
Ratcliff O,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            YU G.
PINEDA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     KEDDIE J.
ADAM L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RIECHMANN J L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MENDEL BIOTECHNOLOGY INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PILGRIM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GACAAGTTCTGCAAGGGGACTGGCGGACGATCTCGCGCAACTTCGTCATCTCGCGGACG
                                                                                                                                                                                                                                                                                                                                                    Page
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CCGACGCAGGTGGCGAGCCACGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CCAACGCAGGTGGCGAGCCACGC 570
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2001WO-US026189.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (first entry)
                                                                                                                                                                                                                                                                                                                                                       527-528;
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                                                                                                                                                                                                                                                                                                                                                  941pp;
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ber JL, Riechmann JL,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ВÞ
                                                                                                                                                                                                                                                                                                                                                    English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Jiang C,
Yu G,
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                                                                                                                                                                                                                                                                                                                                                                                                                             produce a transgenic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Keddie J;
Pineda O;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Keddie
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Query Match 8.9%; Score 118.6; DB 6; Length 867; Best Local Similarity 67.8%; Pred. No. 4e-10; Matches 166; Conservative 0; Mismatches 79; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     recombinant polynucleotide is used for producing a plant having a modified trait, the method comprising selecting a polynucleotide that encodes a polypeptide or an antisense nucleic acid, inserting the polynucleotide or antisense nucleic acid into an expression vector, introducing the vector into a plant or a cell of a plant to overexpress the polypeptide or antisense nucleic acid, thereby producing a modified plant, and selecting for a modified trait (e.g. increased production of agriculturally useful proteins or metabolic chemicals, pest tolerance, environmental stress response (e.g. drought), microbial disease resistance, herbicide resistance, seed and fruit yield, growth rate, leaf and flower senescence and many other traits listed in the specification). The present sequence is one of the 232 polynucleotides encoding an A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 867 BP; 243 A; 189 C; 251 G; 184 T; 0 U; 0 Other;
                                                                                                                                                   576
636 GGAGG 640
                                                                                                                                                                                                                                                                                                          516
                                                                                                                                                                                              598 CATGAACCGCGACCGCCGCCGCCACGACATCCACGACATCACCCAGCGTCACCGCCGGCGA 657
                                                                                                                                                                                                                                                                                                                                                 538 CTCGCGGACGCCAACGCAGGTGGCGAGACCACGCGCAGAAGTACTTCATCCGCCTCAACTC 597
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           418 GGCGGAGCAGGAGAGGCGCAAGGGCATCCCATGGACGGAGGAAGAGCACAGGCTGTTCTT 477
                                                                       658 TCAGG 662
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            478 GCTGGGGCTGGACAAGTTCGGCCAAGGGGGACTGGCGGAAGCATCTCGCGCAACTTCGTCAT 537
                                                                                                                                                                                                                                                                                                                                                                                                                                                     456 AATGGGTTTGAAGAAATATGGGAAAGGAGAGTTGGAGAAACATATCTCGGAACTTTGTGAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            396 GCCGGAGCTGGAGCGGAAGAAAGGCGTTCCTTGGACGGAAGAAGAACACAAGCTATTTCT
                                                                                                                                                   CGGCGGCAAGGACAAGACGAGCAAGCATTCACGACATAACCACCGTAAATCTCGAAGA
                                                                                                                                                                                                                                                                                                  AACGCGAACGCCAACACGAAGTAGCTAGCCACGCCCAAAAAGTACTTCATCCGGCAACTTTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   <u>,</u>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                  575
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Search completed: July 29, 2005, 19:30:58 Job time: 790 secs

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Maximum Match 100%
Listing first 45 summaries
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                                                                    Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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DB seq length: 2000000000
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1: /cgn2 6/ptodata/1/pubpna/US07 Pt

2: /cgn2-6/ptodata/1/pubpna/US06 NE

3: /cgn2-6/ptodata/1/pubpna/US06 NE

4: /cgn2-6/ptodata/1/pubpna/US07 NE

4: /cgn2-6/ptodata/1/pubpna/US07 NE

6: /cgn2-6/ptodata/1/pubpna/US08 NE

6: /cgn2-6/ptodata/1/pubpna/US08 NE

8: /cgn2-6/ptodata/1/pubpna/US08 NE

9: /cgn2-6/ptodata/1/pubpna/US09 NE

10: /cgn2-6/ptodata/1/pubpna/US09 NE

11: /cgn2-6/ptodata/1/pubpna/US09 NE

13: /cgn2-6/ptodata/1/pubpna/US09 NE

14: /cgn2-6/ptodata/1/pubpna/US09 NE

15: /cgn2-6/ptodata/1/pubpna/US108 NE

16: /cgn2-6/ptodata/1/pubpna/US108 NE

17: /cgn2-6/ptodata/1/pubpna/US108 NE

18: /cgn2-6/ptodata/1/pubpna/US108 NE

19: /cgn2-6/ptodata/1/pubpna/US108 NE

10: /cgn2-6/ptodata/1/pubpna/US108 NE
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                                                                                                                                                                                                              : /cgn2_6/ptodata/1/pubpna/PCT_NEW PUB.seq:*
: /cgn2_6/ptodata/1/pubpna/USO6_NEW PUB.seq:*
: /cgn2_6/ptodata/1/pubpna/USO7_NEW PUB.seq:*
: /cgn2_6/ptodata/1/pubpna/USO7_NEW PUB.seq:*
: /cgn2_6/ptodata/1/pubpna/USO7_NEW PUB.seq:*
: /cgn2_6/ptodata/1/pubpna/USO8_PUBCOMB.seq:*
: /cgn2_6/ptodata/1/pubpna/USO8_PUBCOMB.seq:*
: /cgn2_6/ptodata/1/pubpna/USO8_PUBCOMB.seq:*
: /cgn2_6/ptodata/1/pubpna/USO9A_PUBCOMB.seq:*
: /cgn2_6/ptodata/1/pubpna/USOP_PUBCOMB.seq:*
: /cgn2_6/ptodata/1/pubpna/USOP_PUBCOMB.seq:*
: /cgn2_6/ptodata/1/pubpna/USOOP_PUBCOMB.seq:*
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SUMMARIES
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36.0 33.5 21.8 15.5	100.0	Query e Match Length DB]
918 1299 1516 823 1896	- 1	Length
19 20 20 18 20	19	BB
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Sequence 4, Appli Sequence 168067, Sequence 2650, Ap Sequence 4609, Ap Sequence 184212,	Sequence 1, Appli Sequence 59484, A	Description

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US-10-425-114-19199	US-10-425-115-144205	-424-599-11433	0-008-1187	443-7	-10-425-115-	-425-114-18	-10-425-115-	-10-	-10-412-6998	-10-302-267-15	-10-278-536-18	0-286-264-	-10-425	9-732-	-10-425-115-12	-10-739-930-	-10-437-963-4907	-10-425-115-	-10-425-115-	-10-739-930-	-10-425-114-2	-10-425-115-	-10-425-115-]	-10-425-115-	-10-437-963-	-10-425-115-1	-10-425-115-	-10-437-963-56655	-10-425-	US-10-425-115-52607	-10-425-115-44	US-10-425-115-183317	-10-767-	US-10-425-115-183322	-10-437-963-4702	-10-	US-10-437-963-27578
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ALIGNMENTS

RESULT 1 US-10-630-636-1

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APPLICANT: Yu, Su-May
TITLE OF INVENTION: PLANT MYB GENES
FILE REFERENCE: 08919-088001
CURRENT APPLICATION NUMBER: US/10/630,636
CURRENT FILING DATE: 2003-07-30
PRIOR APPLICATION NUMBER: US 60/399,999
PRIOR FILING DATE: 2002-07-31
NUMBER OF SEQ ID NOS: 21
SOFTWARE: FASTSEQ for Windows Version 4.0
SEQ ID NO 1
밁
                               á
                                                                                                                                                                 ; NAME/KEY: CDS
; LOCATION: (20)...(937)
US-10-630-636-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GENERAL INFORMATION
                                                                             Query Match 100.0%; Score 1330;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1330; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 1, Application US/10630636
Publication No. US20040107456A1
                                                                                                                                                                                                                             LENGTH: 1330
TYPE: DNA
ORCANISM: Oryza sativa (japonica cultivar-group)
FEATURE:
1 GTGCGAGATCCACCACCGATGACCTCCCAGGCGGCGACGACGACGACCACGGCGGCGGC
                      GTGCGAGATCCACCGCGATGACCTCCCAGGCGGCGACGACGACGACCACGGCGGCGGC 60
                                                                                                                            DB 19;
                                                                                  0;
                                                                                    Indels
                                                                                                                          Length 1330;
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GCAGCATTTCTTCCTCCTCCTTTCTTGATGTCATCTTGATTTGTTTCTTTGTGTAGTCGC
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; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT4530_61102C.1
US-10-437-963-59484
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Best Local
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Local Similarity 99.5%;
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                                            GCGGGCCGCCTCCCGCGCTACGCCGGGGAGGAGTCCGCGGCGCCCCGACGGA
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RESULT 3 US-10-630-636-4 ; Sequence 4, Application US/10630636 ; Publication No. US20040107456A1 ; GENERAL INFORMATION: ; APPLICANT: Yu, Su-May ; TITLE OF INVENTION: PLANT MYB GENES ; FILE REFERENCE: 08919-088001 ; CURRENT APPLICATION NUMBER: US/10/630,636	Qy 1280 TGCTGATGTAAATTTGCCAACTGTCTCATTGGACCAAAAAAAA	Qy 1220 TACGTGGTGGCGCCGATCGATGATCTTGCAGGGGTTGCAATTAGGGATTGATT	Qy 1160 TCACGTACACCCGGTGAAAGCTTAGCTCCAAATGTGGATGTAATTAGCAGCGGCCTTCCG 1219	Qy 1100 AGGGATTGGGGATTAAAGGCGAATAAGTAAAGTATTTTGCTGACTGTTTGCAAGTGATCA 1159	Qy 1040 ATCTTGTTCTCACAATCTCACTAATGTAAACATACATAGATCAGATGCCAAGAGTGC 1099	Qy 980 CITICITGAIGICAAICITGAITITGTTCITITGTGTAGTCGCCGGCTCAICGICCCTGAIC 1039	Qy 920 CCGGCCAAGATGCACCAATGACGCGCCATGGACGGACATGAGCAGCATTTCTTCCTCCTC 979	Qy 860 CCGGTGGTGTTCCCGCCGGGCCACGCCGTACGTCGTGCCCGTACCCGGCGCCT 919	Qy 800 AGCGCCGCGCCCATGGGCCACCCCGTCGCCGCCACATGGTGCCCGCCGCCGCCGCCGCACG 859	Qy 740 GGCATGAAGCACCACCACCACCACCACCACCACCACGCGGCGGCG	Qy 680 GCCCCGATCACCGGCCACCAGGCCACGGGCACGGGGGGGG	Qy 620 TCCAGCATCCACGACATCACCAGGGTCACCGGCGGGATCAGGTCGCCGCGCAGCAGGGC 679	Oy 560 GCGAGCCACGCGCAGAAGTACTTCATCCGCCTCAACTCCATGAACCGCGACCGCCGCCGC 619	Qy 500 AAGGGGACTGGCGAGCATCTCGCGCAACTTCGTCATCTCGCGGACGCCAACGCAGGTG 559	Qy 440 GGCATCCCATGGACGGAGGAAGAGCACAGGCTGTTCTTGCTGGGGCTGGACAAGTTCGGC 499	Db 1073 GGCGGCGGGTACGACGGCGGCAAGAGCTGCTCCAAGGCGGAGGAGGAGGCGCAAG 1014
Oy 740 GGCATGAAGCACCACCACCACCACCACCGGGCGGCGCGCCGCCGC	Qy 680 GCCCGATCACCGGCCACCAGGCCACGGGCAACCCCGCGGGGGGGG	Qy 620 TCCAGCATCCACGACTCACCAGCGTCACCGCCGGCGATCAGGTCGCCGCGCGCG	Qy 560 GCGAGCCACGCGCAGAAGTACTTCATCCGCCTCAACTCCATGAACCGCGACCGCCGC 619	Qy 500 AAGGGGACTGGCGAAGCATCTCGCGGAACTTCGTCATCTCGCGGACGCCAACGCAGGTG 559	Qy 440 GGCATCCCATGGACGGAGGAAGAGCACAGGCTGTTCTTGCTGGGGCTGGACAAGTTCGGC 499	Qy 380 GGCGGCGGGTACGACGGCGGCAAGAGCTGCTCCAAGGCGGAGAGAGGCGCAAG 439	Qy 320 GCCGGAGCCGCCGCCGCCGCCGTCCAAGGACCGGCGGACCACCGAGCGCAAGGGC 379	Qy 260 GCGGGCCGCGTCCCGGCTCCCGGGCTACGCCGGGAGAGTCCGCGGGCGCCCGACGGA 319	Qy 200 TCGGCGGAGGAGGTGCCGAGGACGACTACGAGGCGTTGGTGGAGGACGTCGCGGGCCATCGAC 259	Qy 140 GGAGGCGCCCGACGACGACTGGTTCGCCGCGGAGCGTGCCCGGGGGCGAGC 199	Qy 80 GAGGACGACAAGGCGTTCGAGAACGCGCTCGCGGGCTTGCGCGGCGCCGCCGCCGCGGAC 139	Qy 20 ATGACCTCCCAGGCGGCGACGACGACGACGACGACGGCGGCGGCGGC	Query Match 69.0%; Score 918; DB 19; Length 918; Best Local Similarity 100.0%; Pred. No. 4.2e-238; Matches 918; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	; TYPE: DNA; ORGANISM: Oryza Bativa (japonica cultivar-group) US-10-630-636-4	NUMBE SOFTW SEQ ID	; CURRENT FILING DATE: 2003-07-30 ; PRIOR APPLICATION NUMBER: US 60/399,999 ; PRIOR FILING DATE: 2002-07-31

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CCGGTGGTGTTCCCGGCGGGGCCACGCGGCGTACGTCGTCGGCTACCCGGCGCCCT

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APPLICANT: LA ROSA, Thomas J.
APPLICANT: Kovalic, David K.
APPLICANT: Chou, Yihua
APPLICANT: Cao, Yongwei
TITLE OF INVENTION: Nucleic Acid Molecules and
TITLE OF INVENTION: Plants
FILE REFERENCE: 38-21(53222)B
CURRENT APPLICATION NUMBER: US/10/425,115
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEG ID NOS: 369326
SEQ ID NO 168067
LENGTH: 1299
TYPE: DNA
ORGANISM: Zea mays
FEATURE:
COURTE THEOROMATTON: Clone ID: MRT4577 84858C.
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US-10-425-115-168067
; Sequence 168067, Application US/10425115
; Publication No. US20040214272A1
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Best Local Similarity 75.0%;
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                              GCAACTTCGTCATCTCGCGGACGCCAACGCAGGTGGCGAGCCACGCGCAGAAGTACTTCA
                                                                                           ACAGGCTGTTCTTGCTGGGGCTGGACAAGTTCGGCAAGGGGGACTGGCGGAGCATCTCGC
                                                                                                                                                           AGAGCTGCTCCAAGGCGGAGCAGGAGAGGCCAAGGGCATCCCATGGACGGAGGAAGAGC
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                                                                                                                                                                                                           ACGTGGCCGCTATCGAGGCCGGCGCATCCCGCTCCCGCGCTACGCTGGGGAGGAGTCGT
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Pred. No. 2.9e-119;
0; Mismatches 193;
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US-10-739-930-2650

Sequence 2650, Application US/10739930

Publication No. US20040216190A1

GENERAL INFORMATION:
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TITLE OF INVENTION: PULCLEIC ACID MOLECULES AND OTHER MOLECULES ASSOCIATED WITH
TITLE OF INVENTION: PLANTS AND USES THEREOF FOR PLANT IMPROVEMENT
FILE REFERENCE: 38-21(53377)B
CURRENT FILING DATE: 2003-12-18
NUMBER OF SEQ ID NOS: 11088
SEQ ID NO 2650
LENGTH: 1516
TYPE: DNA
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OTHER INFORMATION:
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                                                            CCGCCTGATGATGGCTGGTTCACGGCGCGCTGGTGGCGAGCGTGCC---GGCGCGGACGSCG
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                                                                                                                                                                                                                                                       Score 445.4; DB 20;
Pred. No. 4.3e-110;
1; Mismatches 157;
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APPLICANT: Liu, Jingdong
APPLICANT: Zhou, Yihua
APPLICANT: Kovalic, David K.
APPLICANT: Kovalic, David K.
APPLICANT: Screen, Steven E
APPLICANT: Tabaska, Jack E
APPLICANT: Tabaska, Jack E
APPLICANT: Cao, Yongwei
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21(5313)B
CURRENT APPLICATION NUMBER: US/10/425,114
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 73128
SEQ ID NO 4609
LENGTH: 823
TYPE: DNA
ORGANISM: Zea mays
FEATURE:
FEATURE: TAPORMATION: Close ID: 700307574 FIL
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US-10-425-114-4609
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OTHER INFORMATION: Clone ID: 700397574_FLI
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RESULT 7
US-10-425-115-184212
US-10-425-115-184212, Application US/10425115
Publication No. US20040214272A1
GENERAL INFORMATION:
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With
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APPLICANT: Kovalic, David K.

APPLICANT: Kovalic, David K.

APPLICANT: Chou, Yihua

APPLICANT: Chou, Yihua

APPLICANT: Chou, Yongwei

TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated In TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated In TITLE OF INVENTION: NUMBER: US/10/425,115

CURRENT APPLICATION NUMBER: US/10/425,115

CURRENT FILING DATE: 2003-04-28

NUMBER OF SEQ ID NOS: 369326

SEQ ID NO 184212

LENGTH: 1896

TYPE: DNA

ORGANISM: Zea mays
FEATURE:
NAME/KEY: unsure
LOCATION: (1)..(1896)

OTHER INFORMATION: unsure at all n locations
FEATURE:
OTHER INFORMATION: Clone ID: MRT4577_99589C.1

US-10-425-115-184212
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Best Local Similarity
Matches 417; Conserv
APPLICANT:
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TITLE OF IN
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T: Boukharov, Andrey A.

T: Barbazuk, Brad

T: Li, Ping

INVENTION: Rice Nucleic Acid Molecules and Other Molecules

INVENTION: Plants and Uses Thereof for Plant Improvement
                                                              Kovalic, David F
Zhou, Yihua
Cao, Yongwei
Wu, Wei
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GENERAL INFORMATION:
APPLICANT: LA ROSA, Thomas J
APPLICANT: Kovalic, David K
APPLICANT: Zhou, Yihua
APPLICANT: Cao, Yongwei
APPLICANT: Wu, Wei
APPLICANT: Bukharov, Andre
APPLICANT: Barbazuk, Brad

Andrey

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RESULT 9 US-10-437-963-34443/c

Sequence 34443, Application US/10437963 Publication No. US20040123343A1

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CURRENT FILING DATE: 2003-05-14
NUMBER OF SEQ ID NOS: 204966
SEQ ID NO 27578
LENGTH: 1523
TYPE: DNA
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CAATGGAGATACATCTGCTGCTCAG
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                                                                                                                  CCTGAACTCAATGAACAGAGAGAGGCGGCGATCAAGTATACATGACATAACCAGCGTGAA 1022
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Pred. No. 2.2e-43;
1047
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RESULT 10
US-10-437-963-47024
; Sequence 47024, Application US/10437963
; Publication No. US20040123343A1
; GENERAL INFORMATION:
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; OTHER INFORMATION: Clone ID: PAT_MRT4530_38459C.1
US-10-437-983-34443
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TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21(53221)B
CURRENT APPLICATION NUMBER: US/10/437,963
CURRENT FILING DATE: 2003-05-14
NUMBER OF SEQ ID NOS: 204966
SEQ ID NO 34443
TENOTH: 1140
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ORGANISM: Oryza sativa
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Pred. No. 7.1e-43;
0; Mismatches 285;
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  ; OTHER INFORMATION: US-10-425-115-183322
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                                                 FEATURE:
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US-10-425-115-183322/c

i Sequence 183322, Application US/10425115

publication No. US20040214272A1

GENERAL INFORMATION:
APPLICANT: La Rosa, Thomas J.
APPLICANT: Kovalic, David K.
APPLICANT: Zhou, Yihua
APPLICANT: Cao, Yongwei
TITLE OF INVENTION: Nucleic Acid Molecules a
TITLE OF INVENTION: Nucleic Acid Molecules a
TITLE OF INVENTION INVENTION US/10/425,115
CURRENT APPLICATION NUMBER: US/10/425,115
CURRENT APPLICATION OF SEQ ID NOS: 369326

SEQ ID NO 183322
LENGTH: 1793
TYPE: Num
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TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21(53221)B
CURRENT APPLICATION NUMBER: US/10/437,963
CURRENT FILING DATE: 2003-05-14
NUMBER OF SEQ ID NOS: 204966
SEQ ID NO 47024
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APPLICANT: Kovalic, David
APPLICANT: Zhou, Yihua
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ORGANISM: Oryza sativa
PEATURE:
OTHER INFORMATION: Clone ID: PAT_MRT4530_49833C.1
                                         TYPE: DNA
ORGANISM: Zea mays
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Wu, Wei
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Zhou, Yihua
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Barbazuk, Brad
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ID: MRT4577_98775C.
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Pred. No. 5.4e-41;
D; Mismatches 59
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                                                                                                                                                                                        Sequence 9031, Application US/10767701 Publication No. US20040172684A1 GENERAL INFORMATION:
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Best Local Similarity
APPLICANT: Kovalic, David K.
APPLICANT: Kovalic, David K.
APPLICANT: Zhou, Yihua
APPLICANT: Cao, Yongwei
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof For Plant Improvement
FILE REFERENCE: 38-21(53535)B
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GENERAL INFORMATION:
APPLICANT: La ROSA, Thomas J.
APPLICANT: Kovalic, David K.
APPLICANT: Kovalic, David K.
APPLICANT: Cao, Yihua
APPLICANT: Cao, Yongwei
TITLE OF INVENTION: Nucleic Acid Molecules and Otl
TITLE OF INVENTION: Plants
FILE REFERENCE: 38-21(5322)B
CURRENT APPLICATION NUMBER: US/10/425,115
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 369326
SEQ ID NO 183317
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US-10-425-115-183317
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                                                    ; OTHER INFORMATION: US-10-425-115-183317
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CURRENT FILING DATE: 2004-01-29
NUMBER OF SEQ ID NOS: 63128
SEQ ID NO 9031
LENGTH: 965
TYPE: DNA
ORGANISM: Sorghum bicolor
FEATURE:
Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                        Sequence 183317, Application US
Publication No. US20040214272A1
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Best Local Similarity
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                                                                                                TYPE: DNA
ORGANISM: Zea mays
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                                                                                                                                      LENGTH: 1028
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                                                                  ID: MRT4577_98770C.
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   Score
Pred.
   185.6; DB 20;
No. 8.3e-40;
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                   Length 1028;
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음 성 음
; FEATURE:
; OTHER INFORMATION:
US-10-425-115-440
                                                                                             APPLICANT: LA ROSA, Thomas J.
APPLICANT: Kovalic, David K.
APPLICANT: Zhou, Yihua
ITITLE OF INVENTION: Nucleic Acid Molecules and
TITLE OF INVENTION: Plants
FILE REFERENCE: 38-21(53222)B
CURRENT APPLICATION NUMBER: US/10/425,115
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 369326
                                                                                                                                                                                                                                                                                     RESULT 14
US-10-425-115-440
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                                        SEQ ID NO 440
LENGTH: 2481
TYPE: DNA
ORGANISM: Zea mays
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                                                                                                                                                                                                                                                          Sequence 440, Application US/10425115 Publication No. US20040214272A1
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                                                                           US-10.425-115-52607

(Sequence 52607, Application US/10425115

(Publication No. US20040214272A1

(GENERAL INFORMATION:

(APPLICANT: La Rosa, Thomas J.

APPLICANT: Kovalic, David K.

APPLICANT: Cao, Yongwei

(APPLICANT: Cao, Yongwei

(TITLE OF INVENTION: Nucleic Acid Molecules and TITLE OF INVENTION: Nucleic Acid Molecules and FILE REFERENCE: 38-21(53222)B

(CURRENT APPLICATION NUMBER: US/10/425,115

(CURRENT FILING DATE: 2003-04-28

(NUMBER OF SEQ ID NOS: 369326

SEQ ID NO 52607

(SEQ ID NO 52607

LENGTH: 1893
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             ; OTHER INFORMATION: Clone US-10-425-115-52607
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Best Local Similarity
Matches 361; Conserv
                                        TYPE: DNA
ORGANISM: Zea mays
FEATURE:
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                           ID: MRT4577_147976C.1
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With

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1152 TACCGCTTCGGAAGCGGAGGCTGCGGGAGGCGGCACGGCCGCACCC------
1560 GAGGCCAAGCAGCACCAGCACGGCGCTGGGAACCTG
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                                                CCGCCGCCCATGCATGTACAGCGCCGCGCCCATG 814
                                                                                                      AACGCGCCGGCTCCGGCCGCAGTGGTGATAGGCCGCCCTTCTCGTCGGCGGCGGCGGCC
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Pred. No. 1.7e-38;
0; Mismatches 263;
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              GCCCGCCGGCCATGAAGCACCACCACCACCACCGGGCGGCGGCCGCCGCCCAT 789
                                              CCCAGTCCTCCCTAATCACCAGCCAATCGAACGCACCAGCTCCAGCTCCGGCCGCGGGA 1019
                                                         GCTCCAGCATCCACGACATCACCAGCGTC-----ACCGCCGGCGATCAGGTCGCCGCGC 671
                                                                                                                                         TGGCCAGCCACGCGCAGAAGTACTTCATCAGGCTCAACTCCGGCGGCAAGGACAAGAGGA 899
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Search completed: July 29, 2005, 22:49:37 Job time : 954 secs

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Title:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Issued_Patents NA:*

1: /cgn2_6/ptodata/1/ina/5A_COMB.seq:*

2: /cgn2_6/ptodata/1/ina/5B_COMB.seq:*

3: /cgn2_6/ptodata/1/ina/6A_COMB.seq:*

4: /cgn2_6/ptodata/1/ina/6B_COMB.seq:*

5: /cgn2_6/ptodata/1/ina/PCTUS_COMB.seq:*

6: /cgn2_6/ptodata/1/ina/backfiles1.seq:*
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US-09-640-211A-2013
US-09-640-211A-1420
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US-09-640-211A-1955
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                   Sequence 2013, Ap
Sequence 232, App
Sequence 1484, Ap
Sequence 1666, Ap
Sequence 1250, Ap
Sequence 1250, Ap
Sequence 1943, Ap
Sequence 1960, Ap
Sequence 1955, Ap
Sequence 2038, Ap
Sequence 1369, Ap
Sequence 1366, Ap
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6.0	6.0	6.0	6.0	6.1	6.1	6.1	6.1	6.3	6.3	6.4	6.4	6.4	6.4	6.4	6.4	6.4	6.5
5392	5392	5392	380	3957	2896	1557	332	12001	624	532	38506	38506	38506	36778	11220	332	1931
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US-09-231-818-1	US-08-510-646B-1	US-08-403-852D-1	US-09-640-211A-1932	US-10-237-551-193	US-09-902-540-487	US-09-902-540-6559	US-09-640-211A-1984	US-08-458-568A-11	US-09-640-211A-2059	US-09-640-211A-1284	US-09-657-440-19	US-09-141-908-1	US-09-320-878-19	US-09-105-537-5	US-09-105-537-32	US-09-640-211A-1824	US-09-130-114-2
۲,	Sequence 1, Appli	Sequence 1, Appli	Sequence 1932, Ap	Sequence 193, App	Sequence 487, App	Sequence 6559, Ap	Sequence 1984, Ap	Sequence 11, Appl	Sequence 2059, Ap	Sequence 1284, Ap	Sequence 19, Appl	Sequence 1, Appli	Sequence 19, Appl	Sequence 5, Appli	Sequence 32, Appl	Sequence 1824, Ap	Sequence 2, Appli

ALIGNMENTS

В	Q	Db	ð.	₽	Qy	В	8	DЬ	ν	뫄	δ	Query Match Best Local Matches 26	US-09-640-211 Sequence 20 Patent No. GENERAL INF APPLICANT: APPLIC
383 GAGGAAGAAAGGTAACCCATGGACGGAGGAAGAGCATCGAAGGTTTTTAATTGGTCTCCA 442	430 GAGGCGCAAGGGCATCCCATGGACGGAGGAGGAGGACAGGCTGTTCTTGCTGGGGCTGGA 489	323 CGACGGCTACCTGTCCGACGATCCCGCGCCCGGCTCCCACTCGACCGAC	373 CAAGGGCGGCGGCGGCGGGTACGACGGCGGCAAGAGCTGCTCCAAGGCGGAGCAGGA 429	263 CCACTCCTCGTCCTCCGCCGGCATCCCCGAACCCCCGGCTCCTCCCCGATCGACGGGAG 322	313 CGACGGAGCCGGAGCCGCCGCCGCCGCCGCGCGCGGACGAC	203 AACGGACGGTCGATCATGAAGAAGAGCGCCAGCGTGGGGTGCCTGTCCGCCGCCCACTA 262	253 CATCGACGCGGGCCGCGCCCCCGCGCTACGCCGGGGAGGAGTCCGCGGGCGCCGCC 312	143 CGCGGCGGCGGCGTCGGCCTCCGGCGGGGTGAAGCTGTTCGGGGTTAGGTT 202	193 GGCGAGGTCGGCGGAGGTGCGGAGGCACTACGAGGCGCTGGTGGAGGACGTCGCGGC 252	83 CGGCGGGGGCGGCGGCCCCTCCTCCTCCTCCCCCCCCCC	133 CGCGGACGGACGGCCCCGACGACCGACTGGTTCGCCGCGCCGCGAGCGTGCCCGG 192	Match 8.4%; Score 111.8; DB 4; Length 934; Local Similarity 52.7%; Pred. No. 7.2e-13; Local Similarity 52.7%; Local S	US-09-640-211A-2013 Sequence 2013, Application US/09640211A Patent No. 6833446 GENERAL INFORMATION: APPLICANT: Wood, Marion APPLICANT: Shenk, Michael A. APPLICANT: McGrath, Annette APPLICANT: Glenn, Matthew TITLE OF INVENTION: Compositions and Methods for the TITLE OF INVENTION: Modification of Gene Transcription FILE REFERENCE: 11000.1021C1U CURRENT APPLICATION NUMBER: US/09/640,211A CURRENT APPLICATION NUMBER: US/09/640,211A CURRENT FILING DATE: 2000-08-16 NUMBER OF SEQ ID NOS: 2368 SOFTWARE: FastSEQ for Windows Version 4.0 SEQ ID NO 2013 LENGTH: 934 TYPB: DNA ORGANISM: Eucalyptus grandis US-09-640-211A-2013

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US-09-640-211A-232
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SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 232
LENGTH: 1358
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Best Local Similarity
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APPLICANT: Shenk, Michael A.
APPLICANT: McGrath, Annette
APPLICANT: Glenn, Matthew
TITLE OF INVENTION: Compositions and Methods for the
TITLE OF INVENTION: Modification of Gene Transcripti
FILE REFERENCE: 11000.1021C1U
CURRENT APPLICATION NUMBER: US/09/640,211A
CURRENT FILING DATE: 2000-08-16
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CCGCCGCCGCTCCAGCATCCACGACAT
                                                                                   AACGCAGGTGGCGAGCCACGCGCAGAAGTACTTCATCCGCCTCAACTCCATGAACCGCGA 609
                                                                                                                            GAAATTGGGTAAAGGAGCTGGCGAGGGATAGCTCGTGACTTTGTGACTACAAGGACTCC
                                                                                                                                                                                                                                                                                                                                                                              CATCGACGCGGGCCGCGCTCCCGCGCCCGCGCGACGGGGGAGGAGTCCGCGGCGCCCC 312
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CGCGGCGGCGGCGGCGTCGGCCTCCGGCGGCGGGGGTGAAGCTGTTCGGGGTTAGGTT 337
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GGCGAGGTCGGCGAGGAGGTGCGGAGGCACTACGAGGCGCTGGTGGAGGACGTCGCGGC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AACGCAGGTGGCGAGCCCACGCGCAGAAGTACTTCATCCGCCTCAACTCCATGAACCGCGA 609
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                                                       TACTCAAGTGGCAAGCCATGCCCAGAAGTATTATATCCGGCAGAGTAATGCTGGCCGAAG
                                                                                                                                                          CAAGTTCGGCAAGGGGGACTGGCGGAGCATCTCGCGCAACTTCGTCATCTCGCGGACGCC 549
                                                                                                                                                                                                                                  GAGGCGCAAGGGCATCCCATGGACGGAGGAAGAGCACAGGCTGTTCTTGCTGGGGCTGGA 489
                                                                                                                                                                                                                                                                                                       CAAGGGCGGCG---CGGCGGGTACGACGGCGGCAAGAGCTGCTCCAAGGCGGAGCAGGA 429
                                                                                                                                                                                                                                                                                                                                                                                                                 AACGGACGGGTCGATCATGAAGAAGAGCGCCAGCGTGGGGTGCCTGTCCGCCGCCCACTA 397
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                                                                                                                                                                                                 GAGGAAGAAAGGTAACCCATGGACGGAGGAAGAGCATCGAAGGTTTTTAATTGGTCTCCA
                                                                                                                                                                                                                                                                        CGACGGCTACCTGTCCGACGATCCCGCGCCCGGCTCCCGCTCCAATCGGCGCGTCGA
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Pred. No. 7.8e-13;
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APPLICANT: Wood, Marion
APPLICANT: Shenk, Michael A.
APPLICANT: Shenk, Michael A.
APPLICANT: Glenn, Matthew
ITITLE OF INVENTION: Compositions and Methods for the
ITITLE OF INVENTION: Modification of Gene Transcription
FILE REFERENCE: 11000.1021C1U
CURRENT APPLICATION NUMBER: US/09/640,211A
CURRENT PILING DATE: 2000-08-16
NUMBER OF SEQ ID NOS: 2368
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 1484
LENGTH: 335
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US-09-640-211A-1484
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US-09-640-211A-1420
                                          US-09-640-211A-1484
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CURRENT APPLICATION NUMBER: US/09/640,211A
CURRENT FILING DATE: 2000-08-16
NUMBER OF SEQ ID NOS: 2368
SOFTWARE: PastSEQ for Windows Version 4.0
SEQ ID NO 1420
LENGTH: 349
                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 1484, Application Patent No. 6833446 GENERAL INFORMATION:
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APPLICANT: Wood, Marion
APPLICANT: Shenk, Michael
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity
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Query Match
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                                                                                                                    TYPE: DNA ORGANISM: Eucalyptus grandis FEATURE:
                                                           NAME/KEY: misc feature LOCATION: (1)...(335)
OTHER INFORMATION: n =
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McGrath, Annette
Glenn, Matthew
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US-09-640-211A-1666
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RESULT 6
US-09-640-211A-2058
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GENERAL
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Best Local Similarity
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APPLICANT:
APPLICANT:
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Matches 196; Conservative
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TYPE: DNA
ORGANISM: Pinus radiata
-09-640-211A-1666
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0; Mismatches 95;
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US-09-640-211A-1250
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; ORGANISM: Pinus radiata
US-09-640-211A-2058
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APPLICANT: Wood, Marion
APPLICANT: Shenk, Michae
APPLICANT: McGrath, Anne
APPLICANT: Glenn, Matthe
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                                                                                                                                               Query Match
Best Local :
                                                                                                                                                                                                                                                                         SOFTWARE: FastSEQ for Windows Version SEQ ID NO 1250
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Best Local Similarity 68.9%;
Matches 144; Conservative
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APPLICANT: Shenk, Michael A.
APPLICANT: McGrath, Annette
APPLICANT: Glenn, Matthew
TITLE OF INVENTION: Compositions and Methods for the
TITLE OF INVENTION: Modification of Gene Transcription
FILE REFERENCE: 11000.1021CIU
CURRENT APPLICATION NUMBER: US/09/640,211A
CURRENT FILING DATE: 2000-08-16
NUMBER OF SEQ ID NOS: 2368
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                                                                                                                                                                                                                 TYPE: DNA
ORGANISM: Eucalyptus
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143 GGCGCGCCCGACGACGACTGGTTCGCCCGCGCGCGCGACGCGTGCCCGGGGCGAGGTCG
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Glenn, Matthew
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                                                        GIGGCGAGCCACGCGCAGAAGTACTICATCCGCCTCAACTCCATGAACCGCGACCGCCGC 616
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Pred. No. 1.5e-11;
D; Mismatches 247;
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Pred. No. 1.3e-11;
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; ORGANISM: Eucalyptus
US-09-640-211A-1243
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US-09-640-211A-1243
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                                                                                                                                                                                                                                              Query Match 7.3%;
Best Local Similarity 66.0%;
Matches 140; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: McGrath, Annette APPLICANT: Glenn, Matthew
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APPLICANT: Shenk, Michael A.
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Pred. No. 5.7e-10;
0; Mismatches 72;
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Sequence 1960, Application US/09640211A

Patent No. 6833446

GENERAL INFORMATION:

APPLICANT: Wood, Marion
APPLICANT: Shenk, Michael A.

APPLICANT: Mood, Marion
APPLICANT: Mood, Matchev
ITILE OF INVENTION: Compositions and Methods for the
ITILE OF INVENTION: Modification of Gene Transcription
FILE REFERENCE: 11000.1021C1U
CURRENT APPLICATION NUMBER: US/09/640,211A
CURRENT APPLICATION NUMBER: US/09/640,211A
CURRENT FILING DATE: 2000-08-16
NUMBER OF SEQ ID NOS: 2368
SOFTMARE: FastSEQ for Windows Version 4.0
SEQ ID NO 1960
LENGTH: 599
TYPE: DNA
ORGANISM: Eucalyptus grandis
US-09-640-211A-1960
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Best Local Similarity 51.3%;
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                                                                                                               GCGGACGCCAACGCAGGCGAGCCACGCGCAGAAGTACTTCATCCGCCTCAACTCCAT
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CAATCGC
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Pred. No. 7.3e-10;
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US-09-616-289-48/c
US-09-616-289-48/c
; Sequence 48, Application US/09616289
; Patent No. 6632923
; GENERAL IMPORMATION:

592 600 540 472 480 412 420 352 360 292 300 232 240 176

APPLICANT: APPLICANT:

Law, Simon W. Arjona, Anibal

APPLICANT: Lees, Ann M. APPLICANT: Lees, Rober APPLICANT: Law, Simon

Robert ŝ

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CURRENT FILING DATE: 2000-07-14
PRIOR APPLICATION NUMBER: US 09/517,849
PRIOR FILING DATE: 2000-03-02
PRIOR APPLICATION NUMBER: US 08/979,608
PRIOR FILING DATE: 1997-11-26
PRIOR APPLICATION NUMBER: US 60/031,930
PRIOR APPLICATION NUMBER: US 60/048,547
PRIOR PILING DATE: 1997-06-03
PRIOR PILING DATE: 1997-06-03
NUMBER OF SEO ID NOS: 53
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TYPE: DNA
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Best Local (
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FILE REFERENCE: 10797-004001
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Pred. No. 3e-09;
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; TYPE: DNA
; ORGANISM: Eucalyptus
US-09-640-211A-1955
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SOFTWARE: FRANCSCQ for Windows Version 4.0 SEQ ID NO 1955
                                                       Sequence 2038, Application Patent No. 6833446 GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                 Matches 144;
            APPLICANT: Wood, Marion
APPLICANT: Shenk, Mich
APPLICANT: McGrath, An
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Wood, Marion
APPLICANT: Shenk, Mich
APPLICANT: McGrath, An
APPLICANT: Glenn, Matt
   APPLICANT:
                                                                                                                                                               308
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                                                                                                                                                               AAGAAAAAGCGGCGCTCGAGCCTCTTTGACATGGTTGATGTCAAAACCG
                                                                                                                                                                                                                                                                                                           creeacaaerrceecaaeeeeacreeceeaecarcreececaacrreercarcreecee
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McGrath, Annette
Glenn, Matthew
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                                                                                                                                                                                 CGCGACCGCCGCCGCTCCAGCATCCACGACATCACCAGCGTCACCGCCG
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                                                                                                                                                                                                                                                                                CTTGAGAAGCTTGGGAAGGGTGATTGGAGAGGCATCTCTAGGAGCTATGTGACCACAAGA
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연
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McGrath, Annette
Glenn, Matthew
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Pred. No. 2.9e-09;
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Indels

0

Gaps

484

187

247

544

307

356 653

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TITLE OF INVENTION: Compositions and Methods for the TITLE OF INVENTION: Modification of Gene Transcription FILE REFERENCE: 1100.1021CIU
CURRENT APPLICATION NUMBER: US/09/640,211A
CURRENT FILING DATE: 2000-08-16
NUMBER OF SEQ ID NOS: 2368
NUMBER OF SEQ ID NOS: 2368
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 1369
LENGTH: 328
TYPE: DNA
ORGANISM: Eucalyptus grandis
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                                                                                                                                                                                                                                                                                                          Best
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 7.0%;
Best Local Similarity 63.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQ ID NO 2038
LENGTH: 1055
                                                                                                                                                                                                                                                                                                                             Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Matches 142; Conservative
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CURRENT APPLICATION NUMBER: US/09/640,211A
CURRENT FILING DATE: 2000-08-16
NUMBER OF SEO ID NOS: 2368
SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Wood, Marion
APPLICANT: Shenk, Michael A.
APPLICANT: McGrath, Annette
APPLICANT: Glenn, Matthew
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: DNA ORGANISM: Pinus radiata
                                                                                                                                                                                                                                                                                                          Local Similarity
                                          235
                                                                                  545
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              788 AGCAATCTTAATAAAAGGAAACGTCGATCCAGTCTCTTTGATAT 831
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            413 TCCAAGGCGGAGCAGGAGGGCGCAAGGGCATCCCATGGACGGAGGAAGAGCACAGGCTG
                                                                                                                                                                                                                                              425 CAGGAGAGGCGCAAGGGCATCCCATGGACGGAGGAAGAGCACAGGCTGTTCTTGCTGGGG 484
                                                                                                                                                                                                                                                                                       137;
                                                                              ACGCCAACGCAGGTGGCGAGCCACGCGCAGAAGTACTTCATCCGCCTCAACTCCATGAAC
                                                                                                                        CTTGAGAAGCTTGGGAAGGGTGATTGGAGAGGCATCTCTAGGAGCTATGTGACCACAAGA 234
                                                                                                                                                                                                        AACTCCATGAACCGCGACCGCCGCCGCCCAGCATCCACGACAT 636
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CGCGACCGCCGCCGCTCCAGCATCCACGACAT 636
                                        ACACCGGCCCAGGTTGCAAGTCATGCTCAGAAATATTTCCTCCGGCAAGTGAGCTTCAAC
                                                                                                                                                              CTGGACAAGTTCGGCAAGGGGACTGGCGGAGCATCTCGCGCAACTTCGTCATCTCGCGG 544
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                                                                                                                                                                                                                                                                                       Conservative
                                                                                                                                                                                                                                                                                                          64.6%;
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Pred. No. 4.2e-09;
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Pred. No. 3.8e-09;
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GENERAL INFORMATION:

APPLICANT: Wood, Marion
APPLICANT: Mood, Marion
APPLICANT: McGrath, Annette
APPLICANT: McGrath, Annette
ITITLE OF INVENTION: Compositions and Methods for the
ITITLE OF INVENTION: Modification of Gene Transcription
FILE REFERENCE: 11000.1021C1U
CURRENT APPLICATION NUMBER: US/09/640,211A
CURRENT APPLICATION NUMBER: US/09/640,211A
CURRENT FILING DATE: 2000-08-16
NUMBER OF SEQ ID NOS: 2368
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 1966
LENGTH: 427
                                                                                             APPLICANT: McGrath, Annette
APPLICANT: Glenn, Matthew
TITLE OF INVENTION: Compositions and Methods for the
TITLE OF INVENTION: Compositions and Methods for the
TITLE OF INVENTION: Modification of Gene Transcription
FILE REFERENCE: 11000.1021C1U
CURRENT APPLICATION NUMBER: US/09/640,211A
CURRENT FILING DATE: 2000-08-16
NUMBER OF SEQ ID NOS: 2368
NUMBER OF SEQ ID NOS: 2368
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 553
LENGTH: 883
TYPE: DNA
ORGANISM: Pinus radiata
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                                                                                                                                                                                                                                                                                                                                                                                                               Patent No. 6833446 GENERAL INFORMATION:
                     Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 553,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Matches 146;
  Matches 139;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Wood, Marion APPLICANT: Shenk, Mich.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: DNA
ORGANISM: Eucalyptus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TTATATCCGGCAGAGTAATGCTGGCCGAAGAAAGAGGCGCTCCAGCCTTTTTGACAT
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                                                                                                                                                                                                                                                                                                                                                                        Shenk, Michael A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Application US/09640211A
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Conservative
              6.8%;
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Pred. No. 5.9e-09;
0; Mismatches 91
                   Score 90.4; DB 4; Pred. No. 1.1e-08;
  Mismatches
                                        DB 4;
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                                        Length 883;
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Result
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Maximum Match 100%
Listing first 45 summaries
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Maximum DB seq length: 2000000000
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Gapop 10.0 , Gapext 1.0
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Perfect score:
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  1330
1181.2
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 100.0 1330
88.8 142680
87.8 1329
64.0 53000
21.6 187154
14.9 1460
14.9 1465
14.8 1988
13.5 1792
110.6 198102
110.4 126532
110.4 138467
110.2 1161
9.7 928
9.7 1593
9.6 1030
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Match Length DB
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10887.893 Million cell updates/sec
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1330
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Direct Submitsed (10-7AN-2002) Takuji Sasaki, National Institute of Direct Submitted (10-7AN-2002) Takuji Sasaki, National Institute of Agrobiological Sciences, Rice Genome Research Program; Kannondai 2-1-2, Tsukuba, Ibaraki 305-8602, Japan (E-mail:tsasaki@nias.affrc.go.jp, URL:http://rgp.dna.affrc.go.jp/, Tel:81-298-38-7441, Fax:81-298-38-7468)

On Jul 17, 2002 this sequence version replaced gi:19773519.
Genes were predicted from the integrated results of the following: Genes were predicted from the integrated results of the following: (October 1998 version). The genomic sequence was searched against NCBI NonRedundant Protein database, nr
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Oryza sativa (japonica cultivar-group)
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gene		CDS	gene			CDS	200					CDS	gene				CDS	gene				CDS	gene								CDS	gene
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complement (join (39042. .39137

41257. .41417, 42100. .42248))

/gene="OJ1005 B10.11"

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91.2%;
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D; Mismatches
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RESULT 3
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            AK068565 1329 bp mRNA linear PLN 24-JUL-200 Oryza sativa (japonica cultivar-group) cDNA clone:J013154G12, full
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ACCESSION VERSION KEYWORDS SOURCE ORGANISM Agrobiological Sciences Rice Full-Length cDNA project Team:

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Saito, R., Sasaki, D., Sato, K., Shibata, K., Shinagawa, A., Shiraki, T.,

Yoshino, M. and Hayashizaki, Y. AK068565.1 GI:32978582
FLI_CDNA; CAP trapper.
Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza. The Rice Full-Length cDNA Consortium, National Institute of

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JOURNAL
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JOURNAL
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URL: http://cdna01.dna.affrc.go.jp/cDNA/
NIAS Rice Full-Length cDNA Project Team: Kikuchi,S., Satoh,K.,
Nagata,T., Kawagashira,N., Doi,K., Kishimoto,N., Yazaki,J.,
Ishikawa,M., Yamada,H., Ooka,H., Hotta,I., Kojima,K., Namiki,T.,
Ohneda,E., Yahagi,W., Suzuki,K., Li,C., Ohtsuki,K., Shishiki,T.
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Submitted (05-DEC-2001) Shoshi Kikuchi, National Institute of Submitted (05-DEC-2001) Shoshi Kikuchi, National Institute of Agrobiological Sciences, Department of Molecular Genetics, Head (Laboratory of Gene Expression; 2-1-2 Kannondai, Tsukuba, Ibaraki 105-6602, Japan (E-mail:skikuchi@nias.affrc.go.jp, Tel.81-29-838-7007)
Tel.81-29-838-7007, Fax:81-29-838-7007)
This clone is one of the 28K full-length cDNA clones from japonions
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                                                                                                             /organism="Oryza sativa (
/mol type="mRNA"
/cultivar="Nipponbare"
/db xref="taxon:39947"
/clone="J013154G12"
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Score 1167.2; DB 8;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                        Submitted (19-FEB-2003) Takuji Sasaki, National Institute of Agrobiological Sciences, Rice Genome Research Program; Kannondai 2-1-2, Tsukuba, Ibaraki 305-8602, Japan (E-mail:tsasaki@nias.affrc.go.jp, URL:http://rgp.dna.affrc.go.jp/ Tel:81-298-38-7441, Fax:81-298-38-7468)
On Apr 11, 2003 this sequence version replaced gi:28460672. The orientation of the sequence is from -21M13 to M13rev of the Bi
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Oryza sativa (japonica cultivar-group)
Eukaryota, Viridiplantae, Streptophyta; En
Spermatophyta; Magnoliophyta; Liliopsida;
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BAC clone:B1249E06, complete sequence.
AP006233 BA000010
AP006233.2 GI:29824107
                                                                                                                                                                                                                                                                                                                                                                                                                                              clone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sasaki,T., Matsumoto,T. and Katayose,Y. Oryza sativa nipponbare(GA3) genomic DNA,
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                                                                                                                                                                                                                                             Similarity
                                                        GAAGTACTTCATCCGCCTCAACTCCATGAACCGCGACGCCGCCGCCCCAGCATCCACGA
                                                                                                                      GAGCATCTCGCGCAACTTCGTCATCTCGCGGACGCCAACGCCAGGTGGCGAGCCACGCGCA
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     CATCACCAGCGTCACCGCCGCGATCAGGTCGCCGCGCAGCAGGGCGCCCCGATCACCGG
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/mol type="genomic DNA"
/cultivar="Nipponbare"
/db_xref="taxon:39947"
/chromosome="1"
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Feng,Q., Zhang,Y., Hao,P., Wang,S., Fu,G., Huang,Y., Li,Y., Zhu,J.,
Liu,Y., Hu,X., Jia,P., Zhang,Y., Zhao,Q., Ying,K., Yu,S., Tang,Y.,
Weng,Q., Zhang,L., Lu,Y., Mu,J., Lu,Y., Zhang,L.S., Yu,Z., Fan,D.,
Liu,X., Lu,T., Li,C., Wu,Y., Sun,T., Lei,H., Li,T., Hu,H., Guan,J.,
Wu,M., Zhang,R., Zhou,B., Chen,Z., Chen,L., Jin,Z., Wang,R.,
Yin,H., Cai,Z., Ren,S., Ly,G., Gu,W., Zhu,G., Tu,Y., Jia,J.,
Zhang,Y., Chen,J., Kang,H., Chen,X., Shao,C., Sun,Y., Hu,Q.,
Zhang,X., Zhang,W., Wang,L., Ding,C., Sheng,H., Gu,J., Chen,S.,
Ni,L., Zhu,F., Chen,W., Lan,L., Lai,Y., Cheng,Z., Gu,M., Jiang,J.,
Li,J., Hong,G., Xue,Y. and Han,B.
Sequence and analysis of rice chromosome 4
                                                                                                                                                                                              Oryza sativa (japonica cultivar-group) Oryza sativa (japonica cultivar-group) Oryza sativa (japonica cultivar-group) Eukaryota, Viridiplantae, Streptophyta, En Spermatophyta, Magnoliophyta, Liliopsida, Ehrhartoideae, Oryzeae, Oryza.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        This is a complete sequence. Genes were identified by a combination of several methods: Gene prediction programs including Figenesh (http://www.softberry.com/), genscan (http://CCR-081.mit.edu/GENSCAN.html), GeneMarkHMM (http://genemark.biology.gatech.edu/GeneMark/), tRNAscan-SE (Sean Eddy, http://genome.wustl.edu/eddy/tRNAscan-SE/), searches of the complete sequence against NCBI none redundant protein database (nr (ftp://ncbi.nlm.nih.gov/blast/db) and the EST database at NCGR.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Hong, G.F
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       12447439
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Nature 420 (6913), 316-320 (2002) 22337377
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THTFHLPCGEVAPTLODISYLLGLELAGDAVRPVTTGVDWQDDLTARRLALVQRAPHLP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    clone="OSJNBb0062B06"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                organism="Oryza sativa"
organism="Oryza sativa"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   xref="taxon:39947"
                                                                                                                                 lement (join(10043.
8. .16386,17655. .:
                                                                                                                           . 10336,10864. .1111:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     .5282,5395. .5761,5847. .6161,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (japonica cultivar-group)"
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yrarlcmegipmharteavaakligrspvlcggrkkilmemvvahilaiiaapdppfgv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         complement (join (64764 . .64805, 64958 . .65940, 66221 . .6708 67774 . .67858, 68435 . .68536, 68753 . .69149, 69306 . .69546, 69909 . .70953, 71089 . .71118))
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 complement(join(45605. .45901,46925. .47173,47477. .47612,48065. .48283,49052. .49430,49925. .50168))
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /proteIn_id="CAE04045,2"
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AIQRWDBSALSLLPBYMKKFYBALQNYFRETERQVEASDKYRVTCMKKEFQNLSTYYL
QEFEBHLHQNYKRAFKERVALSTLSSTYVPLLCYTAAVGQGDAVTKESFELTTVRASSYL
ACAKIMRFMNDIAAFKSGRKNKGDAANTVBCYMVENKVTSEVALDKIESMIESEWRTL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /db_xref="UniProt/TremBL:Q7X7F4"
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DNCGNQDHLDDPMLEEAVINYSPDGGPEQQESPVYAPTAEGLAVLQSDVNASASDLIA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 complement (64764.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          gene="OSJNBb0062B06.5"
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Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TCGCGCAACTTCGTCATCTCGCGGACGCCAACGCAGGTGGCGAGCCACGCGCAGAAGTAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GTGCGCAGGCTGTTCTTGCTGGGGCTGGACAAGTTCGGCAAGGGAGACTTGCACAGCATC 57884
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GAGCACAGGCTGTTCTTGCTGGGGCTGGACAAGTTCGGCAAGGGGGGACTGGCGGAGCATC 520
CGCGCCATGGACGGACATGAGCAGCATTTCTTCCTCCTCCTTCTTGATGTCAATCTTGA 1000
                                                                                                                                                                                                                                                                           CCCGTCGCCGGCCACATGGTGCCCGCCGCCGTCGGCACGCCGGTGGTGTTCCCCGCCGGCC 880
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GCCACGGGCAACCCCGCGGCGGCGGCGCCTGGGCCCGCCGGGCATGAAGCACCACCACCAC 760
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AGCGTCACCGCCGGCGATCAGGTCGCCGCGCAGCAGGGCGCCCCGATCACCGGCCACCAG 700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CACCACCCGGGGGGGGGGCGCGCGCGCGCATGGCCATGGGCCATGGGCCAC 820
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TTCATACGCCTCAACTCCATGAACCGCGATCGTCGCCGCCTCCAGCATCCACGACATCACC 57764
                                                                                                                                                            CACGCGCCGTACGTCGCCCGTCGGCTACCCCGGCCCCCCGGCCAAGATGCACCAATGA 940
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DNWLQGVCPKDVSPNLFKLAMRKSRTVNKELLLNSWLFSFRQITNIEQIHELVQLGNM
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DDNYYRLSQSQETRNLSPEEAALHRSLKAKTLGLAALNRIKIRORSRLTMIKEGDANT
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LGMSSFDLSDQEEAITMEELELTIKSLPSKKAPGPDGFISAFYKKCWDLIKHDLFNAV
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                                                                                         CTACCCGGCGCCCTGGCCAAGATGCACCAATGACGAGACCACCCTTGC
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Pred. No. 3.4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   87;
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Team: Kikuchi, Kishimoto, N.,

Satoh, K.,

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VERSION
KEYWORDS
SOURCE
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AK068623
LOCUS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The Rice Full-Length cDNA Consortium, National Institute of Agrobiological Sciences Rice Full-Length cDNA Project Team:, Kikuchi, S., Satoh, K., Nagata, T., Kawagashira, N., Dob, K., Kishimoto, N., Yazaki, J., Ishikawa, M., Yamada, H., Ooka, H., Hotta, I., Kojima, K., Namiki, T., Ohneda, E., Yahagi, W., Suzuki, K., Li, C., Ohtsuki, K., Shishiki, T., Foundation of Advancement of International Science Genome Sequencing & Analysis Group:, Otomo, Y., Murakami, K., Iida, Y., Sugano, S., Fujimura, T., Suzuki, Y., Tsunoda, Y., Kurosaki, T., Kodama, T., Masuda, H., Kobayashi, M., Xie, Q., Lu, M., Narikawa, R., Sujiyama, A., Mizuno, K., Yokomizo, S., Nikura, J., Ikeda, R., Sugiyama, A., Mizuno, K., Yokomizo, S., Nikura, J., Ikeda, R., Ishibiki, J., Kawamata, M., Yoshimura, A., Miura, J., Kawai, J., Carninci, P., Adachi, J., Aizawa, K., Arakawa, T., Fukuda, S., Kagawa, I., Kondo, S., Konno, H., Miyazaki, A., Osato, N., Ota, Y., Yoshino, M. and Hayashizaki, Y. Shinagawa, A., Shiraki, T., Yoshino, M. and Hayashizaki, Y.
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Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
                                                                                                                                                                     Submitted (05-DEC-2001) Shoshi Kikuchi, National Institute of Agrobiological Sciences, Department of Molecular Genetics, Head Laboratory of Gene Expression; 2-1-2 Kannondai, Tsukuba, Ibaraki 305-8602, Japan (E-mail:skikuchi@nias.affrc.go.jp, Tel:81-29-838-7007, Fax:81-29-838-7007) This clone is one of the 28K full-length cDNA clones from japoni.
URL: http://cdna01.dna.affrc.go.jp/cDNA/NIAS Rice Full-Length cDNA Project Team: Nagata,T., Kawagashira,N., Doi,K., Kishim
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Science 301 (5631), 376-379 (2003)
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                                                                                                                                                                                                                                                                                        Adachi, J. Alzawa, K., Akimura, T., Arakawa, T., Carninci, P., Doi, K., Fujimura, T., Fukuda, S., Hanagaki, T., Hara, A., Hashizume, W., Hayashida, K., Hayashida, K., Hayashida, K., Hayashida, K., Hiramoto, K., Hiramoto, K., Hiramota, T., Horti, F., Hotte, I., Iida, J., Iida, Y., Ikeda, R., Imamura, K., Imotani, K., Ishibiki, J., Ishii, Y., Ishiawa, M., Itoh, M., Kagawa, I., Kanagawa, S., Katoh, H., Kawagashira, N., Kawai, J., Kawamata, M., Kikuchi, S., Kishikawa-Hirozane, T., Kishimoto, N., Kobayashi, M., Kikuchi, S., Kushikawa-Hirozane, T., Kishimoto, N., Kobayashi, M., Kodama, T., Kojima, K., Kojima, Y., Kondo, S., Konno, H., Kouda, M., Koya, S., Kurihara, C., Kurosaki, T., Kusumegi, T., Li, C., Lu, M., Masuda, H., Matsubara, K., Matsuyama, T., Miura, J., Miyazaki, A., Miruno, K., Murakami, K., Murata, M., Nagata, T., Nakamura, M., Namiki, T., Narikawa, R., Niikura, J., Nishi, K., Oka, M., Ooka, H., Numasaki, R., Ohneda, E., Ohno, M., Ohtsuki, K., Oka, M., Ooka, H., Osato, N., Ota, Y., Otomo, Y., Ryu, R., Saitoh, H., Sakai, C., Sakai, K., Shinagawa, A., Sano, H., Sasaki, D., Sato, K., Satoh, K., Shibata, K., Shiraki, T., Shishiki, T., Sogabe, Y., Sugano, S., Shibata, K., Suzuki, K., Suzuki, K., Tagami, M., Tagami, Takeda, Y., Yamada, H., Yamamoto, M., Yasunishi, A., Yazaki, J., Yokomizo, S. and
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FLI_CDNA; oligo capping.
Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
Direct Submission
Submitted (27-AUG-2002) Shoshi Kikuchi, National Institute of Submitted (27-AUG-2002) Shoshi Kikuchi, National Institute of Agrobiological Sciences, Department of Molecular Genetics, Hee Laboratory of Gene Expression; 2-1-2 Kannondai, Tsukuba, Ibara 305-8602, Japan (E-mail:skikuchi@nias.affrc.go.jp, Tel:81-29-838-7007)
Tel:81-29-838-7007, Fax:81-29-838-7007)
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Kikuchi,S., Satoh,K., Nagata,T., Kawagashira,N., Doi,K.,
Kishimoto,N., Yazaki,J., Ishikawa,M., Yamada,H., Ooka,H., Hotta,I.,
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Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in Riken Hachi, J., Aizawa, K., Akimura, T., Arakawa, T., Carninci, P., Fukuda, S., Hanagaki, T., Hara, A., Hashizume, W., Hayashida, K., Hayatesu, N., Hiraoka, T., Hori, F., Iida, J., Imamura, K., Imotani, K., Ishii, Y., Itoh, M., Kagawa, I., Kanagawa, S., Katoh, H., Kawal, J., Kishikawa-Hirozane, T., Kojima, Y., Kondo, S., Konno, H., Kouda, M., Nashi, K., Nomura, K., Numasaki, R., Ohno, M., Osato, N., Ota, Y., Saitoh, H., Sakai, C., Sakai, K., Sakazume, N., Sano, H., Sasaki, D., Sato, K., Shibata, K., Shinagawa, A., Shiraki, T., Takahashi, F., Takaku-Akahira, S., Tanaka, T., Tomaru, A., Tagama, T., Waki, K., Yasunishi, A. and Hayashizaki, Y.
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                                                                                                      GTTCTTGCTGGGGCTGGACAAGTTCGGCAAGGGGGGACTGGCGAGCATCTCGCGCAACTT
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                                                             GTTCCTTCTTGGACTTGAGAAGTACGGCAAAGGCGACTGGAGGAGTATCTCAAGAAACTT
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                                                                                                                CE 2 (bases 1 to 1988)

CE 2 (bases 1 to 1988)

RS Adachi, J., Aizawa, K., Akimura, T., Arakawa, T., Carninci, P., Doi, K., Fujimura, T., Fukuda, S., Hanagaki, T., Hara, A., Hashizume, W., Hayashida, K., Hayashizaki, Y., Hayatsu, N., Hiramoto, K., Hiraoka, T., Hori, F., Hotta, I., Iida, J., Iida, Y., Ikeda, R., Imamura, K., Imotani, K., Ishibiki, J., Ishi, Y., Ishikawa, M., Itoh, M., Kagawa, I., Kanagawa, S., Katoh, H., Kawagashira, N., Kawai, J., Kawamata, M., Kikuchi, S., Kishikawa-Hirozane, T., Kishimoto, N., Kobayashi, M., Kodama, T., Kojima, K., Kojima, Y., Kondo, S., Konno, H., Kouda, M., Kodama, T., Kojima, X., Kondo, S., Konno, H., Kouda, M., Mizuno, S., Kurihara, C., Kurosaki, T., Kusumegi, T., Li, C., Lu, M., Masuda, H., Matsubara, K., Murata, M., Nagata, T., Nakamura, M., Namiki, T., Narikawa, R., Nikura, J., Mishi, K., Nomura, K., Numasaki, R., Ohneda, E., Ohno, M., Ohtsuki, K., Oka, M., Ooka, H., Osato, N., Ota, Y., Otomo, Y., Ryu, R., Saltoh, H., Sakai, C., Sakai, K., Sakaine, N., Siriba, K., Suziki, Y., Shishiki, T., Sogabe, Y., Sugano, S., Sugiyama, A., Suzuki, K., Suzuki, Y., Tagami, M., Tagami-Takeda, Y., Takahashi, F., Takaku-Akahira, S., Tanaka, T., Tomaru, A., Toya, T., Tsunoda, Y., Ueda, M., Waki, K., Xie, Q., Yahagi, W., Yamada, H., Yamamoto, M., Yasunishi, A., Yazaki, J., Yokomizo, S. and
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Kurosaki,T., Kodama,T., Masuda,H., Kobayashi, M., Xie,Q., Lu,M.,
Narikawa,R., Sujiyama,A., Mizuno,K., Yokomizo,S., Nikura,J.,
Ikeda,R., Ishibiki,J., Kawamata,M., Yoshimura,A., Miura,J.,
Ikeda,R., Ishibiki,J., Kawamata,M., Yoshimura,A., Miura,J.,
Ikeda,R., Riken, Ryu,R., Ueda,M., Matsubara,K., RIKEN,
Kusumegi,T., Oka,M., Ryu,R., Ueda,M., Matsubara,K., RIKEN,
Kusumegi,T., Carninci,P., Adachi,J., Aizawa,K., Arakawa,T., Fukuda,S.,
Hara,A., Hashidume,W., Hayatsu,N., Imotani,K., Ishii,Y., Itoh,M.,
Kagawa,I., Kondo,S., Konno,H., Miyazaki,A., Osato,N., Ota,Y.,
Saito,R., Sasaki,D., Sato,K., Shibata,K., Shinagawa,A., Shiraki,T.,
Yoshino,M. and Hayashizaki,Y.
Collection, mapping, and annotation of over 28,000 cDNa clones from
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FIL CONA; CAP trapper.
Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
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12869764
Direct Submission
Submitted (05-DEC-2001)
Agrobiological Sciences,
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Kishimoto, N., Yazaki, J., Ishikawa, M., Yamada, H., Ooka, H., Hotta, I.,
Kojima, K., Namiki, T., Ohneda, E., Yahagi, M., Suzuki, K., Li, C.,
Kojima, K., Shishiki, T., Foundation of Advancement of International
Science Genome Sequencing & Analysis Group:, Otomo, Y., Murakami, K.,
Iida, Y., Sugano, S., Fujimura, T., Suzuki, Y., Tsunoda, Y.,
Iida, Y., Sugano, S., Fujimura, T., Suzuki, Y., Tsunoda, Y.,
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Oryza sativa (japonica cultivar-group) cDNA clone:J013135D01,
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Science 301 (5631), 376-379 (2003)
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       Shoshi Kikuchi, National, Department of Molecular
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This clone is one of the 28K full-length cDNA clones from japonica rice.

WRL: http://cdna01.dna.affrc.go.jp/cDNA/
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/mol type="mRNA"
/cultivar="Nipponbare"
/db xref="taxon:39947"
/clone="J013135D01"
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Adachi, J., Aizawa, K., Akimura, T., Arakawa, T., Carninci, P., Doi, K., Fujimura, T., Fukuda, S., Hanagaki, T., Hara, A., Hashizume, W., Hayashida, K., Hayashizaki, Y., Hayatsu, N., Hiramoto, K., Hiraoka, T., Hori, F., Hotta, I., Iida, J., Iida, Y., Ikeda, R., Imamura, K., Imotani, K., Ishibiki, J., Ishii, Y., Ishikawa, M., Itoh, M., Kagawa, I., Kanagawa, S., Katch, H., Kawagashira, N., Kawai, J., Kawamata, M., Kikuchi, S., Kishikawa-Hirozane, T., Kishimoto, N., Kobayashi, M., Kodama, T., Kojima, K., Kojima, Y., Kondo, S., Konno, H., Kouda, M., Kova, S., Kurihara, C., Kurosaki, T., Kusumegi, T., Li, C., Lu, M., Masuda, H., Matsubara, K., Murata, M., Nagata, T., Niura, J., Miyazaki, A., Mizuno, K., Murakami, K., Murata, M., Nagata, T., Nakahama, Y., Nakamura, M., Namiki, T., Narikawa, R., Niikura, J., Nishi, K., Noka, H., Osato, N., Ota, Y., Otomo, Y., Ryu, R., Saitoh, H., Sakai, K., Sakai, K., Sakazume, N., Sano, H., Sasaki, D., Sato, K., Satoh, K., Shibata, K., Shinagawa, A., Shiraki, T., Shishiki, T., Sogabe, Y.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The Rice Full-Length cDNA Consortium, National Institute of Agrobiological Sciences Rice Full-Length cDNA Project Team:, Kikuchi, S., Satoh, K., Nagata, T., Kawagashira, N., Dol, K., Kikhimoto, N., Yazaki, J., Ishikawa, M., Yamada, H., Ooka, H., Hotta, I., Kojima, K., Namiki, T., Ohneda, E., Yahagi, W., Suzuki, K., Li, C., Ohtsuki, K., Shishiki, T., Foundation of Advancement of International Science Genome Sequencing & Analysis Group:, Otomo, Y., Murakami, K., Iida, Y., Sugano, S., Fujimura, T., Suzuki, Y., Tsunoda, Y., Kurosaki, T., Kodama, T., Masuda, H., Kobayashi, M., Xie, Q., Lu, M., Narikawa, R., Sugiyama, A., Mizuno, K., Yokomizo, S., Nikura, J., Ikeda, R., Ishibiki, J., Kawamata, M., Kyoshimura, A., Miura, J., Kusumegi, T., Oka, M., Ryu, R., Ueda, M., Matsubara, K., RIKEN:, Kawai, J., Carninci, P., Adachi, J., Aizawa, K., Arakawa, T., Fukuda, S., Hashidume, W., Hayatsu, N., Imctani, K., Ishii, Y., Itoh, M., Kagawa, I., Kondo, S., Konno, H., Miyazaki, A., Osato, N., Ota, Y., Yoshimo, M. and Hayashizaki, Y.
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Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
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Oryza sativa (japonica cultivar-group)
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Best Local
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FAIS Genome Sequencing & Analysis Group: Otomo, Y., Iida, Y.,
FUJimura, T., Ikeda, R., Ishibiki, J., Kawamata, M.,
Kobayashi, M., Kodama, T., Kurosaki, T., Kusumegi, T., Lu, M.,
Kobayashi, M., Kodama, T., Kurosaki, T., Kusumegi, T., Lu, M.,
Masuda, H., Miura, J., Mizuno, K., Narikawa, R., Niikura, J., Oka, M.,
Ryu, R., Sugano, S., Sugiyama, A., Suzuki, Y., Tsunoda, Y., Ueda, M.,
Xie, Q., Yokomizo, S., Yoshimura, A., Matsubara, K. and Murakami, K.
Genome Exploration Research Group in Riken Genomic Sciences Center
and Genome Science Laboratory in Riken: Adachi, J., Aizawa, K.,
Akimura, T., Arakawa, T., Carninci, P., Fukuda, S., Hanagaki, T.,
Hara, A., Hashizume, W., Hayashida, K., Hayatsu, N., Hiramoto, K.,
Hiraoka, T., Hori, F., Iida, J., Imamura, K., Imotani, K., Ishii, Y.,
Itoh, M., Kagawa, I., Kanagawa, S., Katoh, H., Kawai, J.,
Kishikawa-Hirozane, T., Kojima, Y., Kondo, S., Konno, H., Kouda, M.,
Koya, S., Kurihara, C., Matsuyama, T., Miyazaki, A., Murata, M.,
Nakamura, M., Nishi, K., Nomura, K., Numasaki, R., Ohno, M., Osato, N.,
Sakazume, N., Sano, H., Sasaki, D., Sato, K., Shibata, K.,
Shinagawa, A., Shiraki, T., Sogabe, Y., Tagami, M.,
Tagami-Takeda, Y., Tagawa, A., Takahashi, F.,
Takaku-Akahira, S., Tanaka, T., Tomaru, A., Toya, T., Waki, K.,
                                                                                                                           191
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NIAS Rice Full-Length cDNA Project Team: Kikuchi,S., Satoh,K.,
Nagata,T., Kawagashira,N., Doi,K., Kishimoto,N., Yazaki,J.,
Ishikawa,M., Yamada,H., Ooka,H., Hotta,I., Kojima,K., Namiki,T.,
Ohneda,E., Yahagi,W., Suzuki,K., Li,C., Ohtsuki,K., Shishiki,T.,
Yamamoto,M. and Nakahama,Y.
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This clone is one of the 32K full-length cDNA clones from japonica
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Takaku-Akahira,S.,
Yasunishi,A. and l
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                                                                                                                                                                                  GCCCGACGACGACTGGTTCGCCGCGCTCGCCGCGAGCGTGCCCGGGGGCGAGGTCGGCGGA 207
                                                                                                                                                                                                                                                   GCAGCCGTGCTGGTACTTGCAGGAGCGGCGAGGTGCGGAGGCGTGGTCGGCAGAGGAGAA 190
                                                          GGAGGTGCGGAGGCACTACGAGGCGCTGGTGGAGGACGTCGCGGCCATCGACGCGGGCCG 267
                                                                                                                                                                                                                                                                                                              CAAGGCGTTCGAGAACGCGCTCGCGGCGTTGCGCGGCGCCGCCGCCGCCGCAGGCGCGC 147
                                                                                                                                                                                                                                                                                                                                                                            CGAGGGCAAGATGATGGCAGAGGCGCTTCGGGAGGTGCTACCGCTGCCCTACTTCCCCGG 130
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/mol_type="mRNA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Location/Qualifiers
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/clone="001-030-C10"
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56.0%;
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Pred. No. 3.7e-10;
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                                                                                                                                                                     Agrobiological Sciences Rice Full-Length cDNA project Team:,
Kikuchi,S., Satoh,K., Nagata,T., Kawagashira,N., Doi,K.,
Kikuchi,S., Satoh,K., Nagata,T., Kawagashira,N., Doi,K.,
Kishimoto,N., Yazaki,J., Ishikawa,M., Yamada,H., Ooka,H., Hotta,I.,
Kojima,K., Namiki,T., Ohneda,E., Yahagi,W., Suzuki,K., Li,C.,
Ohtsuki,K., Shishiki,T., Foundation of Advancement of International
Science Genome Sequencing & Analysis Group:, Otomo,Y., Murakami,K.,
Iida,Y., Sugano,S., Fujimura,T., Suzuki,Y., Tsunoda,Y.,
Kirosaki,T., Kodama,T., Masuda,H., Kobayashi,M., Xie,Q., Lu,M.,
Narikawa,R., Sugiyama,A., Mizuno,K., Yokomizo,S., Niikura,J.,
Ikeda,R., Sugiyama,A., Mizuno,K., Yoshimura,A., Miura,J.,
Ikeda,R., Sugiyama,A., Mizuno,K., Yoshimura,A., Miura,J.,
Kusumegi,T., Oka,M., J., Alzawa,K., Arakawa,T., Fukuda,S.,
Hara,A., Hashidume,W., Hayatsu,N., Imotani,K., Ishii,Y., Itoh,M.,
Kagawa,I., Kondo,S., Konno,H., Miyazaki,A., Ogato,N., Ota,Y.,
Saito,R., Sasaki,D., Sato,K., Shibata,K., Shinagawa,A., Shiraki,T.,
Yoshino,M. and Hayashizaki,Y.
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                                                                             japonica rice
Science 301 (5631),
22752273
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The Rice Full-Length cDNA Consortium,
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                                                                                                                                                     Collection, mapping, and annotation
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cDNA clone:J013124L02, full
                                                                                                                                                             over
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                                                                                                                                                             28,000
                                                                                                                                                             cDNA clones
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2 (bases 1 to 1795)
Adachi,J., Aizawa,K., Akimura,T., Arakawa,T., Carninci,P., Doi,K., Adachi,J., Aizawa,K., Akimura,T., Hara,A., Hashizume,W., Fujimura,T., Fukuda,S., Hanagaki,T., Hara,A., Hiramoto,K., Hiraoka,T., Hayashida,K., Hayashizaki,Y., Hayatsu,N., Hiramoto,K., Hiraoka,T., Hori,F., Hotta,I., Iida,J., Iida,Y., Ikeda,R., Imamura,K., Imotani,K., Ishibiki,J., Ishii,Y., Ishikawa,M., Itoh,M., Kagawa,I., Kanagawa,S., Katoh,H., Kawagashira,N., Kawai,J., Kawamata,M., Kikuchi,S., Kishikawa-Hirozane,T., Kishimoto,N., Kobayashi,M.,

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FEATURES
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in Riken: Adachi, J., Alzawa, K., Akimura, T., Arakawa, T., Carninci, P., Fukuda, S., Hanagaki, T., Hara, A., Hashizume, W., Hayashida, K., Hayatsu, N., Hiramoto, K., Hiramoto, K., Itoh, M., Kagawa, I., Kanagawa, S., Katoh, H., Kawai, J., Kishikawa-Hirozane, T., Kojima, Y., Kondo, S., Konno, H., Kouda, M., Koya, S., Kurihara, C., Matsuyama, T., Miyazaki, A., Murata, M., Nakamura, M., Nishi, K., Nomura, K., Numasaki, R., Ohno, M., Osato, N., Ota, Y., Saitoh, H., Sakai, C., Sakai, K., Sakazuma, N., Sano, H., Sasaki, D., Sato, K., Shibata, K., Shinagawa, A., Shiraki, T., Sogabe, Y., Tagami, M., Tagami-Takeda, Y., Tagawa, A., Takahashi, F., Takaka, A., Tanaka, T., Tomaru, A., Toya, T., Waki, K., Yasunishi, A., and Hayashizaki, Y.
                                                                            188
                                                                                                                                399
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                                                                                                                                                                                                                                                                                                                                         334;
                                                                                                                                                                                                                                                                                      83
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       URL: http://cdna01.dna.affrc.go.jp/cDNA/
NIAS Rice Full-Length cDNA Project Team: Kikuchi,S., Satoh,K.,
Nagata,T., Kawagashira,N., Doi,K., Kishimoto,N., Yazaki,J.,
Ishikawa,M., Yamada,H., Ooka,H., Hotta,I., Kojima,K., Namiki,T.,
Ohneda,B., Yahagi,M., Suzuki,K., Li,C., Ohtsuki,K., Shishiki,T. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Submitted (05-DEC-2001) Shoshi Kikuchi, National Institute of Agrobiological Sciences, Department of Molecular Genetics, Head of Laboratory of Gene Expression, 2-1-2 Kannondai, Tsukuba, Ibaraki 305-8602, Japan (B-mail:skikuchi@nias.affrc.go.jp, Tel:81-29-838-7007, Fax:81-29-838-7007)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               This clone is one of the 28K full-length cDNA clones from japonica rice.
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                        ATCCCGGGCAGGTCGAGGTCATGAACCACTTCAGGGACCTCGAGCTCGACGTC
                                                                         CCGCCCGCGACGACGACGACGACTGGTTCGCCGCGCTCGCCGCGAGCGTG
                                                                                                                                                                                                                                     GCGTCGAGGGGGAACTGGTTCATGGCGCGCAAGTGGTCGCCGGAGGAGAACAAGCAGTTC
                                                                                                                                                                                                                                                                                   Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /cultivar="Nipponbare"
/db_xref="taxon:39947"
/clone="J013124L02"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   organism="Oryza sativa/mol_type="mRNA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ocation/Qualifiers
                                                                                                                                                                                                                                                                                                                                                               12.9%;
                                                                                                                                                                                                                                                                                                                                       0;
                                                                                                                                                                                                                                                                                                                                                               Score 171.6; DB 8;
Pred. No. 2.1e-09;
                                                                                                                                                                                                                                                                                                                                       Mismatches 239;
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AUTHORS
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VERSION
KEYWORDS
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AC145389/c
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AUTHORS
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S 밁 გ 밁 ş

Nusbaum, C., Lander, E., Butler, E., Wing, R., Bharti, A.K.,

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RS Birren, B., Nusbaum, C., Lander, E., Abouelleil, A., Allen, N., Anderson, M., Arachchi, H. M., Barna, N., Bastien, V., Bloom, T., Anderson, M., Cook, A., Cooke, B., Camarrata, J., Chang, J., Choepel, Y., Collymore, A., Cook, A., Cooke, P., Corum, B., DeArellano, K., Diaz, J.S., Dodge, S., Dooley, K., Dorris, L., Erickson, J., Faro, S., Ferreira, P., FitzGerald, M., Gago, D., Galagan, J., Gardyna, S., Graham, L., Grand-Pierre, N., Hafez, N., Hagopian, D., Hagos, B., Graham, L., Grand-Pierre, N., Hafez, N., Hagopian, D., Hagos, B., Graham, L., Grand-Pierre, N., Hafez, N., Hagopian, D., Jones, C., Kamat, A., Karatas, A., Kells, C., Landers, T., Levine, R., Lindblad-Toh, K., Liu, X., Lui, A., Mabbitt, R., MacLean, C., Macdonald, P., Major, J., Manning, J., Matthews, C., McCarthy, M., Maldrim, J., Meneus, L., Mihova, T., Mlenga, V., Murphy, T., Naylor, J., Nguyen, C., Nicol, R., Norbu, C., O'Connor, T., O'Donnell, P., O'Neil, D., Oliver, J., Peterson, K., Phunkhang, P., Pierre, N., O'Neil, D., Oliver, J., Peterson, K., Ente, R., Rise, C., Rogov, P., Roman, J., Schauer, S., Schupback, R., Seaman, S., Severy, P., Smith, C., Spencer, B., Stange-Thomann, N., Stojanovic, N., Stubbs, M., Vassiliev, H., Venkataraman, V.S., Viel, R., Vo, A., Wilson, B., Wu, X., Wyman, D., Young, G., Zainoun, J., Zembek, L., Zimmer, A. and Zody, M.
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HTG: HTGS_PHASE2; HTGS_FULLTOP; HTGS_ACTIVEFIN
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Birren,B., Nusbaum,C., Lander,E.,
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                                                                                                                   Direct Submission
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search, 320 Charles Street, Cambridge, MA (bases 1 to 198102)
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                                                                               (01-JUL-2003) Whitehead Institute/MIT Center
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SEQUENCING IN PROGRESS ***, 4
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                                       02141, USA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            This consensus is derived from a shotgun assembly that has been manually curated. It is the best representation of the BAC that we can generate without further laboratory work. The draft assembly has been edited, and if possible, ends identified by vector as well as by BAC end sequences, and contigs ordered and oriented. Bases that are not Ns are either above 020 or manually edited. This assembly was performed with phrap. All trace files for this project are available at the NCBI trace repository (http://www.ncbi.nlm.nih.gov/Traces/trace.fcgi?). An exact list of reads used in this assembly are available at http://www.broad.mit.edu/annotation/plants/maize/randomclones.html.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Submitted (20-JJN-2004) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA On Jun 16, 2004 this sequence version replaced gi:48717652. All repeats were identified using RepeatMasker: Smit, A.F.A. & Green, P. (1996-1997) http://ftp.genome.washington.edu/RM/RepeatMasker.html
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Butler, E and Wing, R: Arizona Genomics Institute, Biolo Sciences West, 448A, P.O. Box 210088, University of Arizona,
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the accession number will be preserved.

1 20266: contig of 20266 bp in length
20267 20366: gap of 100 bp
20367 78634: contig of 58268 bp in length
78635 78734: gap of 100 bp
78735 140318: contig of 61584 bp in length
140319 140418: gap of 100 bp
140419 198102: contig of 57684 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                   NOTE: This is a 'working draft' sequence. It currently consists of 4 contigs. Gaps between the contigs are represented as runs of N. The order of the pieces is believed to be correct as given, however the sizes of the gaps between them are based on estimates that have provided by the submittor.

This sequence will be replaced
                                                                                                                                                                                                                                                                                                                                                                             by the finished sequence as soon as it is available and
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                                                                                                                     Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.

1 (bases 1 to 126532)
Chow,T.-Y., Hsing,Y.-I.C., Chen,C.-S., Chen,H.-H., Liu,S.-M.,
Chao,Y.-T., Chang,S.-J., Chen,H.-C., Chen,S.-K., Chen,T.-R.,
Chao,Y.-T., Cheng,C.-H., Chung,C.-I., Han,S.-Y., Hsiao,S.-H.,
Hsiung,J.-N., Hsu,C.-H., Lin,S.-J., Lin,Y.-C., Wu,S.-W., Yu,C.-Y.,
Tu,S.-W., Mu,H.-P. and Shaw,J.-F.
Submitted (13-AUG-2002) Institute of Botany, Academia Sinica, Section 2, Academia Road, Nankang, Taipei 11529, Taiwan
                                    2 (bases 1 to 126532)
Chow,T.-Y. and Hsing,Y.-I.C.
Direct Submission
                                                                                 Unpublished
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AC130602.5 GI:51556280
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Oryza sativa (japonica cultivar-group) chromosome 5 clone
                                                                                                          Oryza sativa BAC B1122D01 genomic
                                                                                                                                                                                                                                                                                                                                                                                                           complete sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CACAGGCTGTTCTTGCTGGGGCTGGACAAGTTCGGCAAGGGGGGACTGGCGAGGATCTCG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /mol_type="genomic DNA"
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|mol_type="genomic D
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Pred. No. 1.1e-06;
0; Mismatches 184;
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Direct Submission

Submitted (02-OCT-2004) Institute of Botany, Academia Sinica, 128,

Submitted (02-OCT-2004) Institute of Botany, Academia Sinica, 128,

Section 2, Academia Road, Nankang, Taipei 11529, Taiwan

On Aug 26, 2004 this sequence version replaced gi:51339037.

Genes were predicated from the integrated results of the following:

BLASTN2.0, BLASTX2.0, GENSCAN (Chris Burge,

http://genes.mit.edu/GENSCAN.html), Fgenesh

(http://www.tigr.org/softlab/glimmer/glimmer.html), TWINSCAN

(http://www.tigr.org/softlab/glimmer/glimmer.html), The sequence was

searched against the Swiss-Prot+TrENDI protein database, the NCBI

Plant EST database, the TIGR Rice Gene Index and the rice

full-length cDNA database (KOME,

http://cdnaon/dna_affor Go:n/CDNA/) Annotated Genes are named to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                http://cdna01.cha.affrc.go.jp/cDNa/). Annotated genes are named to indicate the level of evidence for their annotation. Genes with similarity to other proteins are named after the database hits. Genes without significant peptide similarity but with BST similarity are named as unknown proteins. Genes without protein or EST similarity, that are predicted by more than two gene prediction programs over most of their length are annotated as hypothetical proteins. This clone overlaps with OSUNBB0012G21 (accession # AC135421) and OJ1576_F01(accession # AC097176).
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Submitted (18-AUG-2004) Institute of Botany, Academia Sinica,
Section 2. Academia Road, Nankang, Taipei 11529, Taiwan
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Chow,T.-Y. and Heing,Y.-I.C.
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                                                                                                                                                                            complement (13596.
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                                                                                                                               /gene="B1122D01.2"
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                                                                                                                                                                                                                                                                                                       /codon_start=1
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                                                                                                                                                                                                                                                                                                                                                                                 gene="B1122D01.1"
                                                                                                                                                                                                                                                                                                                                                                                                                                 note="unknown protein"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           'clone="B1122D01"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         db_xref="taxon:39947"
chromosome="5"
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RPGGLSDTGLAVIGQYSGI I QYMLLGNVGETDDGLI RFALGCENLRKLEHRSCCFSEQ
ALARAIRSMPSLRYVWVQGYKASKTGHDLMLMARPFWNI EFTPPSSENANRMREDGEP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                        42616.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CVDSQAQILAYYSLAGKRSDCPRSVVPLYPA"
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                                                                                                                                                                                                                                                                                                                                                         /note="putative beta-D-glucan exohydrolase"
join(42616. .42977,43075. .43165,43262. .43
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         complement (14489. .15931)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /note="putative LRR-containing F-box protein"
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                                                                                                                                                                                                                                                                   note="similar to rice
                                                                                                                                                                                                                                                                                                                                                                                                                            'gene="B1122D01.6"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                note="similar to rice EST AK101514"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         note="hypothetical protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        gene="B1122D01.4"
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                                                                                                     AC130612 138467 bp DNA linear Oryza sativa (japonica cultivar-group) chromosome 5
*** SEQUENCING IN PROGRESS ***, 4 ordered pieces.
                                              HTG; HTGS_PHASE2.
                                                                AC130612.1 GI:22212963
                                                                                        AC13061
                                                                                                                                                                                                                                                                                                                                                                                                                                    CGCGCACTCCTCCTCCGCCGCCGCCGTCTCGGAGCAGTTCGGCGTGCTCGTCGACGG 56264
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/note="unknown protein"
complement(join(56089. .56560,56666.
/gene="B1122D01.8"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GAAGGGGGSGFTLDWDGGDDPAGLGFKRSCYMVGGKRARGPDQBRKKGVPWTEBEHKL
FLMGLKKYGRGDWRN1SRNFVTSRTPTQVASHAQKYFIRLNSGGKDKRRSSIHDITTV
NLPDDDHGNPSPSPPPSVLTAHSSSSAAAVSEQFGVLVDGKPPPPLGRGAGHHHFMP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /product="unknown protein"
/protein id="AAU90113.1"
/protein id="AAU90113.1"
/db xref="GI:53749253"
/translation="MMKESYMEVLPPAPAHYFVGQAAAAGGWFLPDRRGGGAWSQEE
/translation="MMKESYMEVALLLPGKTVADVMTHYDDLENDVCFIEAGLYPFPHY
NKVFEQALAALDRNDPERWERVALLLPGKTVADVMTHYDDLENDVCFIEAGLYPFPHY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /translation="MLLVEFQICFNFVLLICLDYFVFVLHIQIRAEGRSTINNRIGQA
MIGPFVVSLKSVYQKLKLQVINWCIFMHGLLME"
complement (56089. .57141)
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45797. .46030
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/protein_id="AAU90112.1"
/db_xref="GI:53749252"
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cultivar-group)
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* This sequence will be replaced

* by the finished sequence as soon as it is availabl

* the accession number will be preserved.

1 90592: contig of 90592 bp in length

* 90593 90692: gap of unknown length

* 90693 100409: contig of 9717 bp in length

* 100410 100509: gap of unknown length

* 100510 137114: contig of 36050 pin length

* 137115 137214: gap of unknown length

* 137215 138667: contig of 1253 bp in length.

Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Chow,T.-Y., Hsing,Y.-I.C., Chen,C.-S., Chen,H.-H., Liu,S.-M., Chao,Y.-T., Chang,S.-J., Chen,H.-C., Chen,S.-K., Chen,T.-R., Chen,Y.-L., Cheng,C.-H., Chung,C.-I., Han,S.-Y., Hsiao,S.-H., Hsiung,J.-N., Hsu,C.-H., Huang,J.-J., Kau,P.-I., Lee,M.-C., Leu,H.-L., Li,Y.-F., Lin,S.-J., Lin,Y.-C., Wu,S.-W., Yu,C.-Y., Yu,S.-W., Wu,H.-P. and Shaw,J.-F.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzeae; Oryza.

1 (bases 1 to 138467)
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Chow,T.-Y. and Hsing,Y.-I.C.
Direct Submission
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cgccggccacarggrgcccgccgccgccgrcggcacgccggrgg
                                                                  CAAGCCTCCGCCGCCGCCGCCGCCGCCGCCGCCCGCCACCACCACCTCCATGCCCCATCC 26173
                                                                                                                                                      CGCGCACTCCTCCTCCTCCGCCGCCGCCGTCTCGGAGCAGTTCGGCGTGCTCGTCGACGG
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                                                                                                          CCCGGGCGCGCGCCGCCCATGCCCATGTACAGCGCCGCCCATGGGCCACCCCGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
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/chromosome="5"
/clone="P0485G09"
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/mol_type="genomic DNA"
/cultivar="Nipponbare"
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Pred. No. 2e-06;
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Submitted (07-JAN-2004) Life Sciences, National Lab
Protein Engineering and Plant Genetic Engineering,
University, Beijing 100871, China
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
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Unpublished
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                                                                                                                                                                                                                                    CGGAGGAAGAGCACAGGCTGTTCTTGCTGGGGCTGGACAAGTTCGGCAAGGGGGACTGGC
                                         ACATCACCAGCGTCACC 649
                                                                                                           AGAAGTACTTCATCCGCCTCAACTCCATGAACCGCGACCGCCGCCGCCTCCAGCATCCACG
                                                                                                                                             GAAGCATTTCAAGGAACTTTGTGATCTCAAGAACTCCAACACAAGTTGCAAGTCATGCTC
                                                                                                                                                                                                                                                                                      ATGGAGGAAGAAGTGGTGGCTCGAGAGCTGAGCAAGAGAAAAAAGGGATTCCATGGA
                                                                                                                                                                                                                                                                                                                    ACGACGGCGAAGAGCTGCTCCAAGGCGGAGCAGGAGAGGCGCAAGGGCATCCCATGGA 452
          ACATCACCACTGTGAAC 606
                                                                                                                                                                                                                  CTGAAGAAGAGCATCGGTTGTTTCGTTTTGGGTTTTGGACAAGTTTTGGGAAAGGAGATTGGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CTACGCCCAGGTGAAGATCGAGGCCGGCAATTCGCACGTCG 26132
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L. and Gu,H.
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                                                                                                                                                                                                                                                                                                                                                          Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     and Gu, H.
                                                                                                                                                                                                                                                                                                                                                                                                                                       /translation="mesvvatwsrebekafenaialhcvebeitedqwnkmssmypsk albevkkhyqilledvkaiengdvplpryhhriglivdeaaaaatspanrdsissgss ekkpingtsgissggsaboderkki phteephengdlekgkgdropists revetsrtetundekgksggsoppkis revetsrtetungapattegggdopyvis kinsmirdrrbssihdittungapatteggdopyviskhrpadpopopopoptmaglgmyggapvigopiiappdhmgsavgtpvmlpppmgthradpopopopopopopopoptmaglgmyggapvigopimapphmgsavgtpvmlpppmgthhhhhhhhhligvapvavpavpvpplpqqhpapstmh"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /product="MYB transcription factor"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   locus_tag="At1g49010"
codon_start=1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      locus_tag="At1g49010"
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                                                                                                                                                                                                                                                                                                                                                     Score 135.4; DB 8; Pred. No. 1.7e-05; 0; Mismatches 76;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             National Laboratory
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             REFERENCE
AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      VERSION
KEYWORDS
SOURCE
ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LOCUS
DEFINITION
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AY086906
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                                                                                                           ORIGIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 JOURNAL
MEDLINE
                                           Matches
                                                         Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AUTHORS
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                                                                                                                                                                                                                                                                                                                                                                                          source
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ACGACGGCGAAGAGCTGCTCCAAGGCGGAGCAGGAGAGGGCGCAAGGGCATCCCCATGGA 452
                                         Conservative
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밁

ATGGAGGAAGAAGTGGTGGCTCGAGAGCTGAGCAAGAGAAAAAAGGGATTCCATGGA

478

0

Mismatches

; 1.6e-05; 76; DB 8

Indels Length

0

Gaps

0

Score 135.4; Pred. No. 1.6

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This colone sequence is one of 5,000 Ceres full-length cDNAs made available to TIGR and Genbank. The following quality assessment of this set was done by comparison with known proteins: two percent of the clones are estimated to be 5'-truncated; less than one percent are 3'-truncated; approximately two percent represent alternative splice variants, including unspliced introns and spliced exons; one percent may contain premature stop codons; five percent may have frame shifts in a coding region. A sequence is considered to be 5'-truncated if it lacks the translation initiation start (ATG). A sequence is considered to be 3'-truncated if it lacks the C-terminal end of the encoded protein. Please note that these cDNA sequences are derived from the Ws or LACE cootypes and therefore may contain polymorphisms when compared to sequences from Col-0. Genset carried out the library production and sequencing of the full-length clones. Ceres, Inc. carried out the clustering of the coation/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2 (bases 1 to 1161)
Brover, V., Troukhan, M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; roside; euroside II; Brassicales; Brassicaceae; Arabidopsis.

1 (bases 1 to 1161)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1161 bp mRNA linear PIN:
Arabidopsis thaliana clone 29302 mRNA, complete sequence
AY086906
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Feldmann, K.
Full-Length cDNA from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Haas, B.J., Volfovsky, N., Town, C.D., Troukhan, M., Alexandrov, N., Feldmann, K.A., Flavell, R.B., White, O. and Salzberg, S.L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FLI CDNA.
Arabidopsis thaliana (thale cress)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Malibu, CA 90265, USA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Direct Submission
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Brover, V., Troukhan, M.,
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KHRPAQPQPQPQPQPQQHPPTMAGLGMYGGAPVGQPTIAPPDHMGSAVGTPVMLPPP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /mol_type="mRNA"
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10.2%;
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윩	Ş	뮍	Ş	В	ş	Дb	ş
659	633	599	573	539	513	479	453
ACATCACCACTGTGAAC 675	633 ACATCACCAGCGTCACC 649	599 AAAAATACTTCATCAGGCTTAACTCGATGAACCGAGATAGAAGGCGGTCTAGCATTCACG 658	573 AGAAGTACTTCATCCGCCTCAACTCCATGAACCGCGGCCGCCGCCCGC	GAAGCATTTCAAGGAACTTTGTGATCTCAAGAACTCCAACACAAGTTGCAAGTCATGCTC 598	513 GGAGCATCTCGCGCAACTTCGTCATCTCGCGGACGCCAACGCAGGTGGCGAGCCACGCGC 572	479 CTGAAGAAGAGCATCGGTTGTTTTTTTTTTTTTTTTTTT	CGGAGGAAGAGCACAGGCTGTTCTTGCTGGGGCTGGACAAGTTCGGCAAGGGGGACTGGC 512

Search completed: July 29, 2005, 21:09:51 Job time: 5931 secs

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Regult
No.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -MODEL-frame+ p2n.model -DEV=xlh
-QCCGn2 1/USPTO spool/US10630636/runat 27072005 123227 12166/app query.fasta_1.455
-QA/CGn2 1/USPTO spool/US10630636/runat 27072005 123227 12166/app query.fasta_1.455
-QA/CGn2 1/USTTO-Frantap -SUFFIX=rge -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0
-UNITS=bits -START=1 -END=-1 -MATRIX-blosum62 -TRANS-human40.cdi -LIST=45
-DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFMT=pto -NORM=ext -HBAPSIZE=500 -MINLEN=0 -MAXLEN=200000000
-USER=US10630636 @CGN 1 1_4200 @runat 27072005 123227 12166 -NCPU=6 -ICPU=3
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-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
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Maximum DB seg length: 200000000
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Perfect score:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    OM protein - nucleic search, using frame_plus_p2n model
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   95
                                                                                                                                                                              Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                         Score
1641
1594
1494
1497
                                                                                                                                                                                                                                              GenEmbl: *
1: gb ba: *
2: gbbha: *
3: gb in: *
4: gb om: *
6: gb pat: *
7: gb pt: *
9: gb pt: *
9: gb pr: *
10: gb pt: *
11: gb st: *
11: gb st: *
13: gb un: *
14: gb vi: *
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1641
1 MTSQAATTTTTAAA
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Match Length
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Ygapop 10.0 , Ygapext
Fgapop 6.0 , Fgapext
Delop 6.0 , Delext
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1 142680
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2 53000
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AY151042
AP004611
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AY151042 Oryza sat
AP004611 Oryza sat
AK068565 Oryza sat
AP006233 Oryza sat
                                                                                         Description
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VERSION
KEYWORDS
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AY151042
LOCUS
DEFINITION
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AY151042 AY151042.1 GI:24850302
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Oryza sat	AP003279	AP003279	8	86	4.	399	45
Antirrhin	77454	AY077454	æ	\mathbf{L}	4.		44
Arabidops	72	ATT1E3	8	348	ŗ	•	43
Arabidops	_	AB008271	8	9	5	410.5	42
Zea mays	AC145389	14538	N	810	5	413	41
dop	AY519531	AY519531	8	83	5	420.5	40
88	AL60666	BOOONL	8	150206	5	422	39
Oryza sat	AL73235	G000	N	1.1	5	423	38
Arabidops	AY519530	1953	8	804	s	423	37
Lycopersi	BT012856	BT012856	8	1029	9	428	36
Arabidops		AY084487	œ	1169	9	428.5	35
Arabidops	AY05618	AY056180	œ	1071	٥.	428.5	ų 4
Arabidops		AY091265	8	823	9	428.5	υ U
Arabidops	AY55030	AY550308	œ	792		428.5	32
Lycopersi	•	LES243339	œ	808	•	437	31
a br		AF239956	æ	1204	٥.	438.5	30
Oryza sat	AK11198	AK111988	œ	1502	7.	448	29
Arabidops	AK11813	AK118135	œ	1645	7.	449	28
		BT006122	œ	928	7.	449	27
		AY519529	8	897	7.	449	26
		AY091177	8	679	7.	451	25
		AY050976	8	915	.7	456	24
Arabidops		AY088362	8	892	.7	456	23
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Arabi		BT005473	8	898	.7	457.5	21
Arabidops		AY519533	8		7	457.5	20
Oryza		AC130612	N	138467	8	472.5	19
Oryza sa	AC130602	AC130602	Ф	3	8	472.5	18
Oryza sa	AK067964	796	œ	1795	9	480	17
Glycine	AB083028	830	œ	1243	۰	489	6
Glycine		830	8	1191		492	5
	AK068138	830	œ	1988		497	14
Arabidops	AY072090	720	œ	1593	ω.	633.5	ü
Arabidops	AY096571	(B	œ	928		633.5	12
Arabidops	51953	1953	ထ			633.5	1
C.	1604	2	œ	119091	9	648.5	10
Oryza sat	672	100N	æ	8		663.5	9
dop	8690	869	8	1161	1	678.5	œ
	952	1952	œ	945	41.3	678.5	7
za e	0616	9190	œ	1465		704.5	σ
Oryza sat	62	AK068623	œ	1460		704.5	v

ALIGNMENTS

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Location/Qualifiers	FEATURES	
Sinica, Taipei, Nankang 115, Taiwan		•
Submitted (17-SEP-2002) Institute of Molecular Biology, Academis	JOURNAL	
Direct Submission	TITLE	
Lu, C.A., Ho, T.H., Ho, S.L. and Yu, S.M.	AUTHORS	
2 (bases 1 to 1330)	REFERENCE	
12172034	PUBMED	
22163024	MEDLINE	
Plant Cell 14 (8), 1963-1980 (2002)	JOURNAL	
and Hormone Regulation of alpha-Amylase Gene Expression		
Three Novel MYB Proteins with One DNA Binding Repeat Mediate Sugar	TITLE	
Lu, C.A., Ho, T.H., Ho, S.L. and Yu, S.M.	AUTHORS	
l (bases 1 to 1330)	REFERENCE	
Ehrhartoideae; Oryzeae; Oryza.		
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;		
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;		
Oryza sativa (japonica cultivar-group)	ORGANISM	
Oryza sativa (japonica cultivar-group)	SOURCE	

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SerSerIleHisAspIleThrSerValThrAlaGlyAspGlnValAlaAlaGlnGlnGly
                                                                                                                                    AlaSerHisAlaGlnLysTyrPheIleArgLeuAsnSerMetAsnArgAspArgArgArg
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                                                          TCCAGCATCCACGACATCACCAGCGTCACCGCCGGCGATCAGGTCGCCGCGCAGCAGGGC
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OGAPITGHQATGNPAAAALGPPGMKHHHHHPGGAPPPMPMYSAAPMGHPVAGHMVPA
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TITLE
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Katayose, Y., Wu, J., Miimura, Y., Cheng, Z., Nagamura, Y.,
Antonio, B.A., Kanamori, H., Hosokawa, S., Masukawa, M., Arikawa, K.,
Chiden, Y., Hayashi, M., Okamoto, M., Ando, T., Aoki, H., Arita, K.,
Hamada, M., Harada, C., Hijishita, S., Honda, M., Ichikawa, Y.,
Idonuma, A., Iijima, M., Ikeda, M., Ikeno, M., Ito, S., Ito, T., Ito, Y.,
Ito, Y., Iwabuchi, A., Kamiya, K., Karasawa, W., Katagiri, S.,
Ito, Y., Iwabuchi, A., Kamiya, K., Karasawa, W., Katagiri, S.,
Kikuta, A., Kobayashi, M., Kono, I., Machita, K., Maehara, T.,
Mizuno, H., Mairubayashi, T., Mukai, Y., Nagasaki, H., Nakashima, M.,
Ohta, I., Ono, N., Saji, S., Nakai, K., Nabata, M., Shimokawa, T.,
Shomura, A., Song, J., Takazaki, Y., Terasawa, K., Tsuji, K., Waki, K.,
Yamagata, H., Yaman, H., Yamah, K., Yoshihara, R., Yukawa, K.,
Zhong, H., Iwama, H., Endo, T., Ito, H., Hahn, J. H., Kim, H. I., Eun, M. Y.,
Yano, M., Jiang, J. and Gojobori, T.
The genome sequence and structure of rice chromosome 1
NE 2337376
NE 2337376
on Jul 17, 2002 this sequence version replaced gi:19773519.
Genes were predicted from the integrated results of the following:
GENSCANI.0, BLASTNZ.0, BLASTXZ.0 as well as SplicePredictor
(October 1998 version). The genomic sequence was searched against
NCBI NonRedundant Protein database, nr
(ftp://ncbi.nlm.nih.gov/blast/db) and the cDNA sequence database at
RGP. Protein homologies of the coding regions were searched against
NCBI NonRedundant Protein database with BLASTNZ.0. ESTs represent
the identified cDNA sequences using BLASTNZ.0. With the
corresponding DDBJ accession no. and RGP clone ID.
A gene with identity or significant homology to a protein is
classified based on the protein name to indicate the homology level
such as same name, 'putative-' and 'like protein'. A gene without
significant homology to any protein but with EST homology (covering
almost the entire length of partial sequence) is classified as an
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Submitted (10-JAN-2002) Takuji Sasaki, National Institute of Agrobiological Sciences, Rice Genome Research Program; Kannondai 2-1-2, Tsukuba, Ibaraki 305-8602, Japan (B-mail:tsasaki@nias.affrc.go.jp, URL:http://rgp.dna.affrc.go.jp/, Tel:81-298-38-7441, Fax:81-298-38-7468)
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FEATURES
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The orientation of the sequence is from M13 to -21M13 of the BAC clone. This sequence of O31005 B10 clone has an overlap with P0516D04 clone (DDBJ: AP003276) at the position 1 to 103,355 of 5' end. The nucleotide sequence of this BAC clone was generated by combining Monsanto and RGP-Jans sequencing data. Detailed information on overlap and assembly quality together with annotation of this entry is available at http://rgp.dna.affrc.go.jp/GenomeSeq.html.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /organism="Oryza sativa (
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GQGPWPRVPHRAEHETCGLKPREVPGGEAAGGYFSMAGYSRGHRLGVTGRRSLLPNCR
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VDGTEVGAALPVVRRRIWPPRGPVVADLASPRPGGGSGLPEARRWIRPPRAPELL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              note="hypothetical protein"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               clone="0J1005_B10"
oin(3399. .3512,4006. .4227,4265. .4328,4613. .4792,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ocation/Qualifiers
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xref="GI:21902093"
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                                                _start=1
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                                                                                                                                                                          .24398,24894. .25130)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      .17014,17370. .17504,18435.
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                                                                                                                          .25130)
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gene

CDS

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codon_start=1

note="hypothetical protein"

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gene

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CDS

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	0	, Qy 26
HishishishishisProGlyGlyAlaProProProMetProMetTy 260	SHISHISHISH CCACCACCACC	Qy 24 Db 13979
GlyHisGlnAlaThrGlyAsnProAlaAlaAlaAlaLeuGlyProPr 240	0 yAlaProIleThrGlyHisGlnAlaTh	Qy 22 Db 13973
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149	9	Оу 14
hrGluGluHis149 GGAGGAAGAGCACAGGTACGCGCGATTCCGGAAATCAAGACGAGCA 139437	1 GlyIleProTrpThrGluGluGluHis	Qy 14: Db 13937
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(P004611 (1-142680)	611 (1-1	US-10-630-63
18e-57 Length: 142680 44.00 Matches: 306 18% Conservative: 0 18% Mismatches: 0 14% Indels: 41 Gaps: 1	res: 1.08e-57 1594.00 arity: 88.18% milarity: 88.18% 97.14%	Alignment Sco Pred. No.: Score: Percent Simil Best Local Si Query Match: DB:

Qy 41 GlyGlyAlaProAspAspTrpPheAlaAlaLeuAlaAlaSerValproGlyAlaArg 60 185	ed. No.: 3.36e-55 Length: 284 ore: 284 rcent Similarity: 92.81\$ st Local Similarity: 92.81\$ ery Match: 1329 1.04\$ 1.04\$ 1.04\$ 1.04\$ 1.050-636-7 (1-306) x AK068565 (1-1329) 1.04\$ 1.04\$ 1.04\$ 1.04\$ 1.04\$ 1.04\$ 1.050-636-7 (1-306) x AK068565 (1-1329) 2.050-636-7 (1-306) x AK068565 (1-1329) 2.050-636-7 (1-306) x AK068565 (1-1329) 2.050-636-7 (1-306) x AK068565 (1-1329) 3.050-636-7 (1-3	URL: http://cdna01.dna.affrc.go.jb/cDNA/ NIAS Rice Pall-Length cDNA Project Team: Kikuchi, S., Satch, K., Nagata, T., Kawagashira, N., Doi, K., Kishimoto, N., Yazaki, J., Ishikawa, M., Yamada, H., Ooka, H., Hotta, I., Kojima, K., Namiki, T., Ohneda, E., Yahagi, W., Suzuki, K., Li, C., Ohtsuki, K., Shishiki, T., Ohneda, E., Yahagi, W., Suzuki, K., Li, C., Ohtsuki, K., Shishiki, T., and Yamamoto, M. PAIS Genome Sequencing & Analysis Group: Otomo, Y., Iida, Y., Pujimura, T., Ikeda, R., Ishibiki, J., Kawamata, M., Kobayashi, M., Kodama, T., Kurosaki, T., Kusumegi, T., Lu, M., Masuda, H., Miura, J., Mizuno, K., Narikawa, R., Nikura, J., Oka, M., Ryu, R., Sugano, S., Yoshimura, A., Matsubara, K. and Murakami, K. Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in Riken Genomic Sciences Center and Genome Science Laboratory in Riken Genomic, K., Ishii, Y., Hiraoka, T., Hori, F., Iida, J., Hayatsu, N., Hiramoto, K., Nikura, T., Carninci, P., Fukuda, S., Hanagaki, T., Kishikawa-Hirozane, T., Kojima, Y., Kondo, S., Konno, H., Kouda, M., Koya, S., Kurihara, C., Matsuyama, T., Miyazaki, A., Murata, M., Koya, S., Kurihara, C., Matsuyama, T., Miyazaki, A., Murata, M., Sasaki, D., Satco, K., Shihara, K., Sakazume, N., Sano, H., Sasaki, D., Satco, K., Shihagawa, A., Shiraki, T., Takaku-Akahira, S., Tanaka, T., Tomaru, A., Toya, T., Waki, K., Yasunishi, A., and Hayashizaki, Y., Shihagawa, A., Shiraki, T., Waki, K., Yasunishi, A., and Hayashizaki, Y., Coline="Notation" Organism="Notation" Or	Tel:81-29-838-7007, Fax:81-29-838-7007) This clone is one of the 28K full-length cDNA clones from japonica rice.
Published Only in Database (2003) REFERENCE 2 (bases 1 to 53000) AUTHORS Sasaki, T., Matsumoto, T. and Katayose, Y. TITLE Direct Submission JOURNAL Agrobiological Sciences, Rice Genome Research Program; Kannondai 2-1-2, Tsukuba, Ibaraki 305-8602, Japan (E-mail:tsasaki@nias.affcc.go.jp, URL:http://rgp.dna.affrc.go.jp/, Tel.81-298-38-7441, Fax:81-298-38-7468) COMMENT On Apr 11, 2003 this sequence version replaced gi:28460672. The orientation of the sequence is from -21M13 to M13rev of the BAC clone. FEATURES Location/Qualifiers 1. 53000 /organism="Oryza sativa (japonica cultivar-group)" /mol type="genomic DNA" /cultivar="Nipponbare"	APO06233 APO0023 APO06233 APO0023 APO06233 APO0023 APO06233 APO0023 APO00233 APO0	Qy 14. GlylleproTrpThrColucludHsArgLeupPhteuLeuGlyLeuAspLysPheGly 15. GGCATCCCATGGACGAGGAGGAGAGACCACAGGCTGTTCTGCTGGCGACAAGTTCCGC 514 Qy 16. LysGlyAspTrpArgSsr1leSerArgAsnPheValleSerArgThrProThrGlnVal 515. AAGGGGACTCCCATGGCGAAGACTCTCGCGCAACTTCGCCGACCACGCCAGGTG 516. LysGlyAspTrpArgSsr1leSerArgAsnPheValleSerArgThrProThrGlnVal 517. AAGGGGGACTGCGCGAAGATCTCGGCGAACTTCGTCATCTCGCGAACCCAAGGTG 518. AlaSerHisAlaGlnLysTyrPheIleArgLeuAsnSerMetAsnArgAspArgArgArgArg 639. CCAGGCCACGCCAGAAGTACTTCATCTCATCCATGAACCGCGACCGCCGCGC 630. CO 631. AlaSerHisAlaGlnLysTyrPheIleArgLeuAsnSerMetAsnArgAspArgArgArg 631. CCAGGCCACGCCAGAAGTACTTCATCTCATCCATGAACCGCGACCGCCGCCGC 632. CCAGGCCACCACCACCACCACCACCACCCACCCACCCAC	Db 395 GGCGGCGGGTACGACGGCGGCAAGAGCTGCTCCAAGGCGGAGAGGCGGAAGAGCGCAAG 454

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DB:
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The Rice Full-Length cDNA Consortium, National Institute of Agrobiological Sciences Rice Full-Length cDNA Project Team:, Kikuchi, S., Satoh, K., Nagata, T., Kawagashira, N., Doi, K., Kishimoto, N., Yazaki, J., Ishikawa, M., Yamada, H., Ooka, H., Hotta, I., Kojima, K., Namiki, T., Ohneda, E., Yahagi, W., Suzuki, K., Li, C., Ohtsuki, K., Shishiki, T., Foundation of Advancement of International Science Genome Sequencing & Analysis Group: Otomo, Y., Murakami, K., Iida, Y., Sugano, S., Fujimura, T., Suzuki, Y., Tsunoda, Y., Kurosaki, T., Kodama, T., Masuda, H., Kobayashi, M., Xie, Q., Lu, M., Narikawa, R., Sugiyama, A., Mizuno, K., Yoshimura, A., Miura, J., Ikeda, R., Ishibiki, J., Kawamata, M., Yoshimura, A., Miura, J., Kusumegi, T., Oka, M., Ryu, R., Ueda, M., Matsubara, K., RIKEN:,
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Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
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/chromosome="1"
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Matches:
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                                                                                                                              FEATURES
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source

/organism="Oryza sativa (
/mol type="mRNA"
/cultivar="Nipponbare"
/db xref="taxon:39947"
/clone="J013153N23"

cultivar-group) "

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                                                                                             Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in Riken Adachi, J., Aizawa, K., Akimura, T., Arakawa, T., Carninci, P., Fukuda, S., Hanagaki, T., Hara, A., Hashizune, W., Hayashida, K., Hayatsu, W., Hiramcto, K., Itoh, M., Ragawa, I., Kanagawa, S., Katoh, H., Kawai, J., Itoh, M., Ragawa, I., Kanagawa, S., Katoh, H., Kawai, J., Kishikawa-Hirozane, T., Kojima, Y., Kondo, S., Konno, H., Kouda, M., Koya, S., Kurihara, C., Matsuyama, T., Miyazaki, A., Murata, M., Koya, S., Kurihara, C., Matsuyama, T., Miyazaki, R., Ohno, M., Osato, N., Nakamura, M., Nishi, K., Nomura, K., Numasaki, R., Ohno, M., Osato, N., Ota, Y., Saitoh, H., Sakai, C., Sakai, K., Sakazume, N., Sano, H., Sasaki, D., Sato, K., Shibata, K., Shinagawa, A., Shiraki, T., Sasaki, D., Sato, K., Tagami, M., Tagami-Takeda, Y., Tagawa, A., Takahashi, F., Takaku-Akahira, S., Tanaka, T., Tomaru, A., Toya, T., Waki, K.,
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This clone is one of the 28K full-length cDNA clones from japonica
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Collection, mapping, and annotation of over 28,000 cDNA clones from
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                                                         ProProGlyHisAlaproTyrValVal----
                                                                                                                                                                                                                                                                                                         AAGCAGTCTCTACAGCCAGCAAATGCGCCTCCAGGCGTCGATGCTTATGGTACGACA---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GluGluSerAlaAlaProProAspGlyAla-----GlyAlaAlaAlaAlaAlaAlaSer 108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CTGGTGGAGGACGTCGACGGCATCGAGGCCGGCGGGTGCCGCTCCTGGTGTACGCCGGC
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704.50
58.57%
51.71%
42.93%
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                                                                                                                                                                                                                                                                                                                                                                                                                                  CCATCAGCA------AATCCTGGAAAATCCTCT
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                                                                                                                                                                                                                                                         CB 2 (bases 1 to 1465)

Adachi, J., Aizawa, K., Akimura, T., Arakawa, T., Carninci, P., Doi, K., Pujimura, T., Fukuda, S., Hanagaki, T., Hara, A., Hashizume, W., Fujimura, T., Fukuda, S., Hanagaki, T., Hara, A., Hashizume, W., Hayashida, K., Hayashizaki, Y., Hayatsu, N., Hiramoto, K., Hiraoka, T., Hori, F., Hotta, I., Iida, Y., Iida, Y., Ikeda, R., Imamura, K., Immotani, K., Ishibiki, J., Ishii, Y., Ishikawa, M., Itoh, M., Kagawa, I., Kanagawa, S., Katoh, H., Kawagashira, N., Kawai, J., Kawamata, M., Kanagawa, S., Kishikawa-Hirozane, T., Kishimoto, N., Kobayashi, M., Kodama, T., Kojima, Y., Kondo, S., Konno, H., Kouda, M., Kodama, T., Kojima, Y., Kondo, S., Konno, H., Kouda, M., Kodama, T., Kojima, Y., Kondo, S., Konno, H., Kouda, M., Kodama, T., Muraka, M., Mizuno, K., Murakami, K., Murata, M., Nagata, T., Nakamura, M., Namiki, T., Narikawa, R., Niikura, J., Nishi, K., Nomura, K., Numasaki, R., Ohneda, E., Ohno, M., Ohtsuki, K., Oka, M., Ooka, H., Osako, N., Ota, Y., Otomo, Y., Ryu, R., Saitch, H., Sakai, C., Sakai, K., Sakazume, N., Sano, H., Sasaki, D., Satoh, K., Sabata, K., Shinagawa, A., Shiraki, T., Shishiki, T., Sogabe, Y., Sugano, S., Sugiyama, A., Suzuki, K., Suzuki, Y., Tagami, M., Tagami, Takeda, Y., Yamada, H., Yamamoto, M., Yasunishi, A., Yazaki, J., Yokomizo, S. and Yoshia, H., Yamamoto, M., Yasunishi, A., Yazaki, J., Yokomizo, S. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Agrobiological Sciences Rice Full-Length cDNA project Team., Kikuchi, S., Satoh, K., Nagata, T., Kawagashira, N., Dob, K., Kishimoto, N., Yazaki, J., Ishikawa, M., Yamada, H., Ooka, H., Hotta, I., Kojima, K., Namiki, T., Ohneda, E., Yahagi, W., Suzuki, K., Li, C., Ohtsuki, K., Shishiki, T., Foundation of Advancement of International Science Genome Sequencing & Analysis Group:, Otomo, Y., Murakami, K., Iida, Y., Sugano, S., Fujimura, T., Suzuki, Y., Teunoda, Y., Kurosaki, T., Kodama, T., Masuda, H., Kobayashi, M., Xie, Q., Lu, M., Narikawa, R., Sugiyama, A., Mizuno, K., Yokomizo, S., Nikura, J., Ikeda, R., Ishibiki, J., Kawamata, M., Yoshimura, A., Miura, J., Kusumegi, T., Oka, M., Ryu, R., Ueda, M., Matsubara, K., RIKEN:, Kawai, J., Carninci, P., Adachi, J., Aizawa, K., Arakawa, T., Fukuda, S., Kagawa, I., Kondo, S., Konno, H., Miyazaki, A., Osato, N., Ota, Y., Saito, R., Sasaki, D., Sato, K., Shibata, K., Shinagawa, A., Shiraki, T., Yoshimo, M. and Hayashizaki, Y.
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                         Submitted (27-AUG-2002) Shoshi Kikuchi, National Institute of Agrobiological Sciences, Department of Molecular Genetics, Head Laboratory of Gene Expression; 2-1-2 Kannondai, Tsukuba, Ibaraki 305-8602, Japan (E-mail:skikuchi@nias.affrc.go.jp, Tel:81-29-838-7007, Fax:81-29-838-7007)
This clone is one of the 28K full-length cDNA clones from japoni
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Collection, mapping, and annotation of over 28,000 cDNA clones from japonica rice Science 301 (5631), 376-379 (2003) 22752273
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AK106166.1 GI:32991375
FII_CNNA; oligo capping.
Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Em
Spermatophyta; Magnoliophyta; Liliopsida;
Ehrhartoideae; Oryzeae; Oryza.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AK106166 1465 bp mRNA linear PLN 24-JUL-2003 Oryza sativa (japonica cultivar-group) cDNA clone:001-208-B07, full
                                                                                                                                                                                                               Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The Rice Full-Length cDNA Consortium,
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a; Poales; Poaceae;
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from japonica

of.

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Percent Similarity:
Best Local Similarity:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FAIS Genome Sequencing & Analysis Group: Otomo, Y., Iida, Y.,
Fujimura, T., Keda, R., Ishibiki, J., Kawamata, M., Kobayashi, M.,
Kodama, T., Kurosaki, T., Kusumegi, T., Lu, M., Masuda, H., Miura, J.,
Kodama, T., Kurosaki, T., Kusumegi, T., Lu, M., Masuda, H., Miura, J.,
Mizuno, K., Narikawa, R., Niikura, J., Oka, M., Ryu, R., Sugano, S.,
Sugiyama, A., Suzuki, Y., Tsunoda, Y., Ueda, M., Xie, Q., Yokomizo, S.,
Sugiyama, A., Matsubara, K. and Murakami, K.
Genome Exploration Research Group in Riken Genomic Sciences Center
and Genome Science Laboratory in Riken: Adachi, J., Aizawa, K.,
Akmura, T., Azakawa, T., Carninci, P., Fukuda, S., Hangaki, T.,
Akmura, T., Azakawa, T., Garninci, P., Fukuda, S., Hangaki, K.,
Hara, A., Hashizume, W., Hayashida, K., Hayatsu, N., Hiramoto, K.,
Hiraoka, T., Hori, F., Iida, J., Imamura, K., Imotani, K., Ishii, Y.,
Itoh, M., Kagawa, I., Kanagawa, S., Katchh, H., Kawai, J.,
Itoh, M., Kagawa, I., Kanagawa, S., Katchh, H., Kawai, J.,
Nakamura, M., Nishi, K., Nomra, T., Myazaki, A., Murata, M.,
Nakamura, M., Nishi, K., Nomra, T., Myazaki, A., Ohno, M., Osto, N.,
Ota, Y., Saitoh, H., Sakai, C., Sakai, K., Sakazume, N., Sano, H.,
Sasaki, D., Sato, K., Shibata, K., Shinagawa, A., Takhashi, F.,
Takaku-Akahira, S., Tanaka, T., Tomaru, A., Toya, T., Waki, K.,
Yasunishi, A., and Hayashizaki, Y.
                                                                            540
                                                                                                                  109
                                                                                                                                                        501
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                                                                                                                                                                                                                                                                                                               384 CTAGCGGAGGCCGTGGAGGGG---AAGACGGCCGACGAGGTGAGGCGGCACTACGAGCTG 440
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NIAS Rice Full-Length cDNA Project Team: Kikuchi,S., Satoh
Nagata,T., Kawagashira,N., Doi,K., Kishimoto,N., Yazaki,J.
Ishikawa,M., Yamada,H., Ooka,H., Hotta,I., Kojima,K., Nami
Ohneda,E., Yahagi,W., Suzuki,K., Li,C., Ohtsuki,K., Shishi
                          Lys-----SerCysSerLysAlaGluGlnGluArgArgLysGlyIleProTrp 144
                                                                                                      LysåspGlyGlyHisårgårgåspGluårgLysGlyGlyGlyGlyGlyTyråspGlyGly 128
                                                                                                                                                                                                                                  CTGGTGGAGGACGTCGACGCATCGAGGCCGGGCGGCGGCTCCTGGTGTACGCCGGC 500
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CATGGGGAGAAGGGGTCGGCTAAGTCCTCTGAGCAGGAGCGCCCGGAAGGGGGATCGCCTGG
                                                                                                                                                                                                                                                           LeuValGluAspValAlaAlaIleAspAlaGlyArgValProLeuProArgTyrAlaGly
                                                                                                                                                                                            GluGluSerAlaAlaProProAspGlyAla------GlyAlaAlaAlaAlaAlaSer 108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /organism="Oryza sativa
/mol_type="mRNA"
/cultivar="Nipponbare"
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/clone="001-208-B07"
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704.50
58.57%
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                                                                                                                                                        GACGGGGGCGTCGAGGAGGGCTCTGCGGGAGGTGGGAAG 539
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Shishiki,T. a
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/locus_tag="At1g49010"
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Direct Submission
Submitted (07-JAN-2004) Life Sciences, National Laboratory of Submitted (07-JAN-2004) Life Sciences, National Laboratory of Protein Engineering and Plant Genetic Engineering, Peking University, Beijing 100871, China
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/organism="Arabidopsis thaliana"
/mol_type="mRNA"
/db_xref="taxon:3702"
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KHRPAQPQPQPQPQPQHHPPTMAGLGMYGGAPVGQPIIAPPDHMGSAVGTPVMLPPP
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                                                                                                                                  gg
                                                                                                                                                                                                                                         source
                                                                                                                                                                                                                                                                           Malibut CA 90265, USA

This clone sequence is one of 5,000 Geres full-length cDNAs made
available to TIGR and Genbank. The following quality assessment of
this set was done by comparison with known proteins: two percent
are 3'-truncated; approximately two percent represent alternative
splice variants, including unspliced introns and spliced exons; one
percent may contain premature stop codons; five percent may have
frame shifts in a coding region. A sequence is considered to be
5'-truncated if it lacks the translation initiation start (ArG). A
sequence is considered to be 3'-truncated if it lacks the translation please note that these cDNA
sequences are derived from the Ws or LAer ecotypes and therefore
may contain polymorphisms when compared to sequencing of the
full-length clones. Ceres, Inc. carried out the clustering of the
full-length clones. Selection of clones, and sequence assembly.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           259
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Arabidopsis thaliana clone 29302
AY086906.1 GI:21405616
FLI_CDNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicoty; core eudicots; rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.

1 (bases 1 to 1161)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        3 (bases 1 to 1161)
Brover, V., Troukhan, M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Full-Length cDNA from Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Haas, B.J., Volfovsky, N., Town, C.D., Troukhan, M., Alexandrov, N., Feldmann, K.A., Flavell, R.B., White, O. and Salzberg, S.L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Arabidopsis thaliana (thale Arabidopsis thaliana
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Submitted (11-MAR-2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Feldmann, K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Brover, V.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Genome Biol. 3 (6),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              annotation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Full-length messenger RNA sequences greatly improve
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/codon_start=1
/product="unknown"
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/protein_id="AAM69950.1"
/db_xreft="GI:21555865"
/translation="MESVVATWSREEEKAFENAIALHCVEEEITEDQWNKMSSMVPSK
/translation="MESVVATENGQVPLPRYHHRKGLIVDEAAAAATSPANRDSHSSGSS
                                                                                                                                                    /organism="Arabidopsis
/mol_type="mRNA"
/db_xref="taxon:3702"
/clone="29302"
                                                                                                                                                                                                                                                           ocation/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Troukhan, M.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Alexandrov, N., Lu, Y.-P.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           cress)
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US-10-630-636-7 (1-306) x AY086906
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DB:
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Best Local Similarity:
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                                                                                                                                                                                                                                                                                                                                                          AlaSerHisAlaGlnLysTyrPheIleArgLeuAsnSerMetAsnArgAspArgArgArg
                                                                                                                                                                                                                                                                                                                                                                                                                                            LysGlyAspTrpArgSerIleSerArgAsnPheValIleSerArgThrProThrGlnVal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GlyIleProTrpThrGluGluHisArgLeuPheLeuLeuGlyLeuAspLy8PheGly
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GlyGlyGlyGlyTyrAspGlyGlyLysSerCysSerLysAlaGluGluGluArgArgLys
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TCTCATTCCTCTGGATCATCTGAGAAGAAACCAAATCCTGGCACCTCCGGGATAAGTAGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LeuAlaAlaSerValProGlyAlaArgSerAlaGluGluValArgArgHisTyrGluAla 71
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AlaAlaAlaAlaAtaTrpThrArgGluAspAspLysAlaPheGluAsnAlaLeuAlaAla
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GlyHisArg-----ArgAspGluArgLy8-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CGCAAAGGTCTCATCGTAGATGAAGCAGCAGCAGCAGCTACTTCTCCTGCCAACAGAGAC 354
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CTTTTAGAAGATGTCAAAGCAATCGAGAATGGTCAAGTTCCTTTACCTCGTTATCATCAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LeuValGluAspValAlaAlaIleAspAlaGlyArgValProLeuProArgTyrAlaGly 91
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ATGTCGTCAATGGTACCA---AGCAAAGCCTTAGAAGAAGTAAAGAAACATTACCAAATC 234
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AGTGTGGTGGCAACATGGAGCAGAGAAGAAGAAAGCATTCGAGAACGCAATTGCGTTG
GGGATGTATGGTGGTGCGCCAGTGGGACAACCGATCATCGCACCAGCTGATCATATG---
                                                                                                                                                                                                                                                                    SerSerIleHisAspIleThrSerValThrAlaGlyAspGlnValAlaAlaGlnGlnGly
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GGGATTCCATGGACTGAAGAAGAGCATCGGTTGTTTCTTTTGGGTTTTGGACAAGTTTTGGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TCCAATGGAGGAAGAAGTGGTGGC--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GluGluSerAlaAlaProProAspGlyAlaGlyAlaAlaAlaAlaAlaSerLysAspGly 111
                                                                               CCGCAACCACAACATCAT--
                                                                                                                      GlyMetLysHisHisHisHisHisProGlyGlyAlaProProProMetPro----
                                                                                                                                                                                                      AlaProIleThrGlyHisGlnAlaThrGlyAsnProAlaAlaAlaAlaLeuGlyProPro
                                                                                                                                                                 GGAGGACAACAACCGCAAGTGGTTAAAACATAGACCAGCCTCAGCCACAACCACCACAACAA
                                                                                                                                                                                                                                                                                                                                                                                                                AAAGGAGATTGGAGAAGCATTTCAAGGAACTTTGTGATCTCAAGAACTCCAACACAGATT
                                      MetTyrSerAlaAlaProMetGlyHisProValAlaGly-----
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RNFVISRTPTQVASHAQKYFIRLNSMIRDRRRSSIHDITTVNNQAPAVTGGGQQPQVV
KHRPAQPQDPQPQQAHPPTWAGLGNYGGAPVGQPIIAPPDHMGSAVGTPVMLPPP
MGTHHHHHHHHLGVAPYAVPAYPVPPLPQQHPAPSTWH"
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678.50
58.44%
49.06%
41.35%
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Matches:
Conservative:
Mismatches:
Indels:
Gaps:

    ACTGTGAACAATCAAGCTCCTGCGGTTACAGGA

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                                                                               CCCCCAACAATGGCTGGATTA
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14
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JOURNAL
MEDLINE
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On Jul 9, 2003 rhin
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Liu,Y., Hu,X., Jia,P., Zhang,Y., Zhao,Q., Ying,K., Yu,S., Tang,Y.,
Weng,Q., Zhang,L., Lu,Y., Mu,J., Lu,Y., Zhang,L.S., Yu,Z., Fan,D.,
Liu,X., Lu,T., Li,C., Wu,Y., Sun,T., Lei,H., Li,T., Hu,H., Guan,J.,
Wu,M., Zhang,R., Zhou,B., Chen,Z., Chen,L., Jin,Z., Wang,R.,
Yin,H., Cai,Z., Ren,S., Lv,G., Gu,W., Zhu,G., Tu,Y., Jia,J.,
Zhang,Y., Chen,J., Kang,H., Chen,X., Shao,C., Sun,Y., Hu,Q.,
Zhang,Y., Zhang,W., Wang,L., Ding,C., Sheng,H., Gu,J., Chen,S.,
Ni,L., Zhu,F., Chen,W., Lan,L., Lai,Y., Cheng,Z., Gu,M., Jiang,J.,
Li,J., Hong,G., Xue,Y. and Han,B.
Sequence and analysis of rice chromosome 4
Native Ago, (cail) 216-270 (2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Han, B., Feng, Q., Huang, Y.C., Li, Y., Zhu, J.J., Zhao, Q., Hu, X., Liu, Y.L., Mu, J., Yu, Z., Chen, L., Fan, D.L., Weng, Q.J., Zhang, L., Lu, Y.C., Li, C., Li, T., Zhang, Y.J., Lu, Y., Li, C., Li, T., Zhang, Y.J., Lu, Y., Li, C., Chen, Z.H., Hao, P., Zhang, L., Wu, M., Zhang, R.Q., Guan, J.P., Fu, G., Wang, S.Y., Ren, S.X., Lv, G., Lin, W., Gu, W.Q., Zhu, G.F., Tu, Y.F., Jia, J., Yin, H.F., Zhang, Y., Cai, Z., Chen, J., Kang, H., Chen, X.Y., Shao, C.Y., Sun, Y., Hu, Q.P., Zhang, X.L., Zhang, W., Wang, L.J., Shao, C.Y., Sheng, H.H., Gu, J.L., Chen, S.T., Ni, L., Zhu, F.H. and Chen, G.F., Shang, H.H., Gu, J.L., Chen, S.T., Ni, L., Zhu, F.H. and
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Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; hiliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
                                                                                                                                                                                                                       This is a complete sequence. Genes were identified by a combination of several methods: Gene prediction programs including Egenesh (http://www.softberry.com/), genscan (http://CCR-081.mit.edu/GENSCAN.html), GeneMarkHWM (http://genemark.biology.gatech.edu/GeneMarkh/), tRNAscan-SE (Sean Eddy, http://genome.wustl.edu/eddy/tRNAscan-SE/), searches of the complete sequence against NCBI none redundant protein database (ftp://ncbi.nlm.nih.gov/blast/db) and the EST database at NCGR.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 On Jul 9, 2003 this sequence version Web site: http://www.ncgr.ac.cn
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Submitted (08-SEP-2001) Han Bin, National Center for Gene Chinese Academy of sciences, 500# Cao Bao Road, Shanghai 2 CHINA. E-mail enquiries: bhan@ncgr.ac.cn. Clone requests:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Nature 420 (6913), 316-320 (2002)
22337377
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GGTTCAGCTGTTGGAACACCTGTGATGCTTCCACCTCCAATGGGAACTCATCATCATCAC
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                                                                                                                                                                                                Location/Qualifiers
                                                                                                                                                                   .187154
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BAC clone: OSJNBb0062B06,
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RGGGGGDGDVGRRSGAATGRLEBAGGMGGRRGGRRGGRRGTHYBLKRLKRENGRRGFHFI
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6241. .6561,6647. .6799)
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                                                                                                                                                                   gene="OSJNBb0062B06.5"
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gene

SGC

US-10-630-636-7 (1-306) x OSJN00107 (1-187154)

Query Match:

Percent Similarity: Best Local Similarity:

2.84e-18 663.50 65.00% 63.75% 40.43%

Conservative: Mismatches: Indels:

13 73 8 Length: Matches:

Gaps:

Alignment Scores: Pred. No.:

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                                                      Shinn, P., Brooks, S., Buehler, E., Chao, Q., Johnson-Hopson, C., Khan, S., Kim, C., Altafi, H., Bei, Q., Chin, C., Chiou, J., Choi, E., Conn, L., Conway, A., Gonzales, A., Hansen, N., Howing, B., Koo, T., Lam, B., Lee, J., Lenz, C., Li, J., Liu, A., Liu, K., Liu, S., Mukharsky, N., Nguyen, M., Palm, C., Pham, P., Sakano, H., Schwartz, Southwick, A., Thaveri, A., Toriumi, M., Vaysberg, M., Yu, G., Federspiel, N. A., Theologis, A. and Ecker, J. R.

Genomic sequence for Arabidopsis thaliana BAC F27J15 from
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Submitted (70-NOV-1999) Directity of Pennsylvania, 38th Str
Department of Biology, University of Pennsylvania, 38th Str
Hamilton Walk, Philadelphia, Pennsylvania 19104-6018, USA
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Department of Biology, University of Pennsylvania, 38th
Hamilton Walk, Philadelphia, PA 19104-6018, USA
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hpvllteaplnekanrekmtqimfetfnspamyvaiqavlsluxasgrttgivldssdi
vshtvpiybgofslphailkldlagrdltdylmkiltzegymftttaereivrdikekl
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PERKYSVWIGGSILASLSTFQOMWISKAEYDEAGPGIVHRKCF"
complement(join(9639. .9780,9817. .10114,11072. .11183,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              complement (join (1671. .1736, 1844. .2457, 2554.
                                                                                                                           note="putative RING zi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /protein_id="AAF69724.1"
/db_xref="GI:7770354"
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/product="F27J1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /clone="F27J15"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /organism="Arabidopsis thaliana"
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/db_xref="taxon:3702"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Location/Qualifiers
                           /evidence=not_experimental
/product="F27J15.2"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   chromosome="1"
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                                                                                                                                                             zinc
                                                                                                                                  finger protein
>|T75752.1"
                                                                                                                                                                 gb|AAF16660.1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Kim, C.,
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SPQFNYLMNNEELLQASGLSATDLELTYPSLPYDPQEYLINGYNYN"
join(32180. 32395,32476. 32593,32673,32608. 3
32944. 33037,33113. 33193,33279. 33390,33706. 33793,
33963. 34029,34381. 34500,34578. 34667,44798. 34866)
note="similar to MAP/ERK kinase kinase 3 gi|4505153"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPVQSDPARSDRLDQVKADFKIVEDEPIINETPLITWTEEIQPVQSDLVQANKFDQV
NGYSEIMNQDNMYNKAPKENTWTEUQPVQSULVQTKEFGQLUDYSQIMNQDSMYN
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NVNTTIPSYLMNGPATLNQIQQNQYQNGFLTWNNQIITNPPPLFYLDHHHQQQHQS
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SPLITHENNLSGNVMMLLSILIGIICCLGLHYIIRCALRRSTRMISBVPSSLSSTR
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RCIDKWLQQHLTCPKCRNCLVETCQKILGDFSQADSVTAEPTEIVIVTIVPLEPTEIV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /translation="MLVGKISGYEDNTRSLERETSEITSLLSQFPGNTNVLVVDTNFT
TLLNMKQIMKQYAYQVSIETDAEKALAFLTSCKHEINIVIWDFHMPGIDGLQALKSIT
SKLDLFVVIMSDDNQTESVMKATFYGACDYVVKPVKEEVMANIWQHIVRKRLIFKPDV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TCQKILGDFSQADSWASTPTESVIVRIDPLEPEGRVNTFRESS"

complement(join(26020. .26439,26567. .26652,26749.
27852. .28004,28099. .28276))

/note="putative two-component response regulator"
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complement(join(16947. .17596,21011. .21320))
/note="putative RING finger protein gb|AAD08934.1;
to EST gb|N37302.1"
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/product="F27J15.4"
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'codon_start=1
                                                                                                                                                                                       protein_id="AAF69697.1"
/db_xref="GI:7770327"
                                                                                                                                                                                                                                                 /evidence=not_experimental
/product="F27J15.6"
                                                                                                                                                                                                                                                                                                                                               note="similar to serine/threonine kinase 9 gb|AAD28798.1"
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/db_xref="GI:7770326"
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                                   141
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GlyIleProTrpThrGluGluGluHis--
                                                                                                TCCAATGGAGGAAGAAGTGGTGGC
                                                                                                                                          GlyGlyGlyGlyTyrAspGlyGlyLysSerCysSerLysAlaGluGlnGlnArgArgLys 140
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gg

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TCGAGAGCTGAGCAAGAGAGAAAA 86509

149

Sas

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US-10-630-636-7 (1-306) x AC016041 (1-119091)
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Query Match:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            86898 AGTGTGGTGGCAACATGGAGCAGAGAAGAAGAAAGCATTCGAGAACGCAATTGCGTTG
                                                                                                                                                                                                                                                                                   72 LeuValGluAspValAlaAlaIleAspAlaGlyArgValProLeuProArgTyrAlaGly 91
                                                                                                                                                                                                                                                                                                                                                                                                                52 LeuAlaAlaSerValProGlyAlaArgSerAlaGluGluValArgArgHisTyrGluAla 71
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              33 ---CysAlaAlaProProProAlaAspGlyGlyAlaProAspAspAspTrpPheAlaAla 51
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          13 AlaAlaAlaAlaAlaTrpThrArgGluAspAspLysAlaPheGluAsnAlaLeuAlaAla 32
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CATTGT-----GTAGAGGAAGAGAGATAACAGAGGATCAATGG---AACAAA 86797
TCTCATTCCTCTGGATCATCTGAGAAAAACCAAATCCTGGCACCTCCGGGATAAGTAGC 86560
                                                       GlyHisArg-----ArgAspGluArgLys-----
                                                                                                                 CGCAAAGGTCTCATCGTAGATGAAGCAGCAGCAGCAGCTACTTCTCCTGCCAACAGAGAC 86620
                                                                                                                                                                        GluGluSerAlaAlaProProAspGlyAlaGlyAlaAlaAlaAlaAlaSerLysAspGly 111
                                                                                                                                                                                                                               ATGTCGTCAATGGTACCA---AGCAAAGCCTTAGAAGAAGTAAAGAAACATTACCAAATC 86740
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MVEQLELTDKNVKFIAELIDVLLVNLIPNWKTDVAVDHLIHPQQNQSSKDNHQNGASS
QAGESISHSLSSDYCPRSDDEANFTVAATTEDQEAEKGSLEEBEEDERLKEELEKIE
ERFREMKEITRKREBATMETKNRFFEKKNQQVE"
complement (join (40641 . 40798, 40897 . .41041))
/note="hypothetical protein"
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join(41349. .41637,41888. .41922)
/note="maimilar to NADH-ubiquinone oxidoreductame 12 kD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            translation="MGRKKGLPEFEESAPDGFDPENPYKDPVAMVEMREHIVREKWIH"
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|db_xref="GI:7770329"
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648.50
51.94%
43.61%
39.52%
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Matches:
Conservative:
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Gaps:
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RESULT 11
AY519532
LOCUS
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AUTHORS
TITLE
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SOURCE
ORGANISM
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TITLE
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                                                                                                                           Direct Submission
Submitted (07-JAN-2004) Life Sciences,
Protein Engineering and Plant Genetic University, Beijing 100871, China
                                                                                                                                                                                                                                                   Qu.L. and Gu,H.
The MYB Transcription Factor Family in Arabidopsis:
                                                                                                                                                                                                                                                                                                                                  Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                Arabidopsis thaliana (thale Arabidopsis thaliana
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AY519532
Arabidopsis thaliana MYB transcription factor (Att
                                                                                                                                                                                                            일,다.
                                                                                                                                                                                                                                           Unpublished
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                                                                                                                                                                                                                                                                                       IleSerArgAsnPheValIleSerArgThrProThrGlnValAlaSerHisAlaGlnLys
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Yamada,K., Banh,J., Chan,M.M., Chang,C.H., Chang,E., Dale,J.M., Deng,J.M., Goldsmith,A.D., Lee,J.M., Onodera,C.S., Quach,H.L., Tang,C., Toriumi,M., Wu,H.C., Yamamura,Y., Yu,G., Bowser,L., Carninci,P., Chen,H., Cheuk,R., Hayashizaki,Y., Ishida,J., Jones,T., Kamiya,A., Karlin-Neumann,G., Kawai,J., Kim,C., Lam,B., Lin,J., Meyers,M.C., Miranda,M., Narusaka,M., Nguyen,M., Palm,C.J., Sakurai,T., Satou,M., Seki,M., Shinn,P., Southwick,A., Shinozaki,K., Davis,R.W., Ecker,J.R. and Theologis,A. Arabidopsis Open Reading Frame (ORF) Clones
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Yamada, K., Banh, J., Chan, M.M., Chang, C.H., Chang, E., Dale, J.M., Deng, J.M., Goldsmith, A.D., Lee, J.M., Onodera, C.S., Quach, H.L., Tang, C.C., Toriumi, M., Wu, H.C., Yamamura, Y., Yu, G., Bowser, L., Carninci, P., Chen, H., Cheuk, R., Hayashizaki, Y., Ishida, J., Jones, T., Kamiya, A., Kariin-Neumann, G., Kawai, J., Kim, C., Lam, B., Lin, J., Meyers, M.C., Miranda, M., Narusaka, M., Nguyen, M., Palm, C.J., Sakurai, T., Satou, M., Seki, M., Shinn, P., Southwick, A., Shinozaki, K., Davis, R.W., Ecker, J.R. and Theologis, A.
                                                                                                                                                                                   The Salk, Stanford, PGEC (SSP) Consortium members constructed and sequenced the pUNI (ORF) clones using the RAFL cDNAs: Yamada, K., Banh, J., Chan, M., Chang, C.H., Chang, B., Dale, J.M., Deng, J.M., Goldsmith, A.D., Lee, J.M., Onodera, C.S., Quach, H.L., Tang, C.C., Toriumi, M., Wu, H.C., Yamamura, Y., Yu, G., Bower, L., Chen, H., Cheuk, R., Jones, T., Karlin-Namann, G., Kim, C., Lam, B., Lin, J., Meyers, M.C., Miranda, M., Nguyen, M., Palm, C.J., Shinn, P., Southwick, A., Davis, R.W., Ecker, J.R. and Theologis, A.
                                                                                                                                                                                                                                                                                                                                                                                                          Submitted (16-APR-2002) Plant Gene Expression Center, 800 Buchanan Street, Albany, CA 94710, USA
The RIKEN Genomic Sciences Center (GSC) members carried out the collection and clustering of RAFL cDNAs (RAFL cDNA: 'RIKEN Arabidopsis Full-Length cDNA'): Seki,M., Narusaka,M., Ishida,J., Satou,M., Kamiya,A., Sakurai,T., Carninci,P., Kawai, J., Hayashizaki,Y. and Shinozaki,K.
                    Annotation is based on the January 2002 version of the Arabidopsis genome submitted to GenBank.
                                                                                        Yamada,K. (SSP/PGEC) and Seki, M. (RIKEN GSC) contributed to this work. Shinozaki,K. (RIKEN GSC) and Theologis,A. (PGEC) contributed equally to this work as PIs.
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                                                     IleSerArgAsnPheValIleSerArgThrProThrGlnValAlaSerHisAlaGlnLys
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                           ATTTCTCGCAACTTTGTAGTAACAAGAACACCGACCCAAGTTGCGAGCCATGCTCAAAAG
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/protein id="ANM2021.1"
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AGGGNKSAKQNSQAPGPPMYGTPAIGQPAVGTPVNLPAPPHMAYGVHAAPVPGSVV
PGAAMNIGQMPYTMPRTPTAHR"
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1 (bases 1 to 1593)

Yamada, K., Liu, S.X., Sakano, H., Pham, P.K., Banh, J., Chung, M.K.,

Goldsmith, A.D., Lee, J.M., Quach, H.L., Toriumi, M., Yu, G., Bowser, L.

Carninci, P., Chen, H., Cheuk, R., Hayashizaki, Y., Ishida, J.,

Jones, T., Kamiya, A., Karlin-Neumann, G., Kawai, J., Kim, C., Lam, B.,

Lin, J., Miranda, M., Narusaka, M., Nguyen, M., Palm, C.J., Sakurai, T.,

Satou, M., Seki, M., Shinn, P., Southwick, A., Shinozaki, K.,

Davis, R.W., Ecker, J.R. and Theologis, A.

Arabidopsis Full Length cDNA Clones

Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Yamada,K., Banh,J., Chan,M.M., Chang,C.H., Chang,E., Dale,J.M., Deng,J.M., Goldsmith,A.D., Lee,J.M., Onodera,C.S., Quach,H.L., Tang,C.C., Toriumi,M., Wu,H.C., Yamamura,Y., Yu,G., Bowser,L., Carninci,P., Chen,H., Cheuk,R., Hayashizaki,Y., Ishida,J., Jones,T., Kamiya,A., Karlin-Neumann,G., Kawai,J., Kim,C., Lam,B., Lin,J., Meyers,M.C., Miranda,M., Narusaka,M., Nguyen,M., Palm,C.J. Sakurai,T., Satou,M., Seki,M., Shinn,P., Southwick,A., Shinnzaki,K., Davis,R.W., Ecker,J.R. and Theologis,A.
The Salk, Stanford, PGEC (SSP) Consortium members carried out the sequencing and annotation of the RAFL CDNAs: Yamada, K., Banh, J., Chann, M.M., Chang, C.H., Chang, E., Dale, J.M., Deng, J.M., Goldsmith, A.D., Lee, J.M., Onodera, C.S., Quach, H.L., Tang, C.C.,
                                                                                                                                                                            Submitted (02-JAN-2002) Plant Gene Expression Center, 800 Buchan Street, Albany, CA 94710, USA RIKEN Genomic Sciences Center (GSC) members carried out the collection and clustering of RAFL cDNAs (RAFL cDNA : 'RIKEN Arabidopsis Full-Length cDNA'): Seki,M., Narusaka,M., Ishida,J., Satou,M., Kamiya,A., Sakurai,T., Carninci,P., Kawai,J., Hayashizaki,Y. and Shinozaki,K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
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Arabidopsis thaliana unknown protein (At5g08520) mRNA, complete
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CGGTGGGAGAAGATTGCTGCAGACGTTCCAGGC---AAAAGTGTTGAACAGATTAAAGAA
                                                                                                                                                                              TrpPheAlaAlaLeuAlaAlaSerValProGlyAlaArgSerAlaGluGluValArgArg
                                                                                                                                                                                                                       AGAGCTCTA-----GCCAATAATACCGATGAATCAGAGGAA
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product="unknown protein"
/protein id="ALIS913.1"
/protein id="ALIS913.1"
/db_xref="GI:18175700"
/translation="MTYDEVESDGSVWSREDDIAFERALANNTDESEERWEKIAADVPG
KSYEQIKEHYELLVEDVTRIESGCVPLPAYCSPEGSNGHAGDEGASSKKGGNSHAGES
NQAGKSKSDQERRKGIAWTEDEHRLFLLGLDKYGKGDWRSISRNEVVTRTPTQVASHA
QKYFILINSMNKDRRSSIHDITSVCANDVSTPQGFITGQNNSNNNNNNNNNNNSSPAV
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/mol_type="mRNA"
/db_xref="taxon:3702"
/chromosome="5"
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Agrobiological Sciences Rice Full-Length cDNA Project Team:, Kikuchi, S., Satoh, K., Nagata, T., Kawagashira, N., Doi, K., Kishimoto, N., Yazaki, J., Ishikawa, M., Yamada, H., Ooka, H., Hotta, I., Kojima, K., Namiki, T., Ohneda, B., Yahagi, W., Suzuki, K., Li, C., Ohtsuki, K., Li, C., Ohtsuki, K., Shishiki, T., Foundation of Advancement of International Science Genome Sequencing & Analysis Group:, Ocomo, Y., Murakami, K., Iida, Y., Sugano, S., Fujimura, T., Suzuki, Y., Tsunoda, Y., Kurosaki, T., Kodama, T., Masuda, H., Kobayashi, M., Xie, Q., Lu, M., Kurosaki, T., Kodama, T., Masuda, H., Kobayashi, M., Xie, Q., Lu, M., Narikawa, R., Sugiyama, A., Mizuno, K., Yokomizo, S., Niikura, J., Ikeda, R., Sugiyama, A., Mizuno, K., Yokohimura, A., Miura, J., Ikeda, R., Sugiyama, A., Kawamata, M., Yoshimura, A., Miura, J., Kawamata, M., Kashimura, A., Miura, J., Kawamata, M., Kashimura, A., RIKEN, Kawai, J., Carninci, P., Adachi, J., Aizawa, K., Arakawa, T., Fukuda, S., Kawai, J., Carninci, P., Adachi, J., Aizawa, K., Arakawa, T., Fukuda, S.,
                                                                                                                                                                                                                                                                                                                                                          AK068138.1 GI:32978156
FLI_CNNA; CAP trapper.
Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
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                                                    /mol_type="mRNA"
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Hayashida, K., Hayashizaki, Y., Hayatsu, N., Hashizume, W.,
Hori, F., Hotta, I., Iida, J., Iida, Y., Ikeda, R., Imamura, K.,
Imotani, K., Ishibiki, J., Ishii, Y., Ishikawa, M., Itoh, M., Kagawa, I.,
Kanagawa, S., Katoh, H., Kawagashira, N., Kawai, J., Kawanata, M.,
Kikuchi, S., Kishikawa-Hirozane, T., Kishimoto, N., Kobayashi, M.,
Kodama, T., Kojima, K., Kojima, Y., Kondo, S., Konno, H., Kouda, M.,
Kodama, T., Kojima, K., Kojima, Y., Kondo, S., Konno, H., Kouda, M.,
Koya, S., Kurihara, C., Kurosaki, T., Kusumegi, T., Li, C., Lu, M.,
Masudda, H., Matsubara, K., Matsuyama, T., Miura, J., Miyazaki, A.,
Mizuno, K., Murakami, K., Murata, M., Nagata, T., Nakamura, M.,
Namiki, T., Narikawa, R., Niikura, J., Nishi, K., Nomura, K.,
Numasaki, R., Ohneda, E., Ohno, M., Ohtsuki, K., Oka, M., Ooka, H.,
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Shinagawa, A., Shiraki, T., Sogabe, Y., Sugano, S.,
Sugiyama, A., Shiraki, T., Siahiki, T., Sogabe, Y., Sugano, S.,
Sugiyama, A., Takahashi, F., Takaka, Takafara, S., Tanaka, T., Tomaru, A.,
Toya, T., Tsunoda, Y., Ueda, M., Waki, X., Xie, Q., Yahagi, W.,
Tarana, A., Yamamoto, M., Yasunishi, A., Yazaki, J., Yokomizo, S., and
                                                                                     and Genome Science Laboratory in Riken: Adachi, J., Aizawa, K., Akimura, T., Arakawa, T., Carninci, P., Fukuda, S., Hanagaki, T., Hara, A., Hashizume, W., Hayashida, K., Hayatsu, N., Hiramoto, K., Hiraoka, T., Hori, F., Iida, J., Imamura, K., Imotani, K., Ishii, Y., Itoh, M., Kagawa, I., Kanagawa, S., Katoh, H., Kawai, J., Kishikawa-Hirozane, T., Kojima, Y., Kondo, S., Konno, H., Kouda, M., Koya, S., Kurihara, C., Matsuyama, T., Myzazaki, A., Murata, M., Nakamura, M., Nishi, K., Nomura, K., Numasaki, R., Ohno, M., Osato, N., Sakani, C., Sakai, K., Sakazume, N., Sano, H., Sakai, C., Sakai, K., Sakazume, N., Satoh, K., Shinagawa, A., Shiraki, T., Sogabe, Y., Tagami, M., Tagami-Takeda, Y., Tagawa, A., Takahashi, F., Takaku-Akahira, S., Tanaka, T., Tomaru, A., Toya, T., Waki, K., Takaki, C., Takaku-Akahira, S., Tanaka, T., Tomaru, A., Toya, T., Waki, K.,
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Fujimura,T., Ikeda,R., Ishibiki,J., Kawamata,M., Kobayashi,M.,
Fujimura,T., Kurosaki,T., Kusumegi,T., Lu,M., Masuda,H., Miura,J.,
Kodama,T., Kurosaki,T., Kusumegi,T., Lu,M., Ryu,R., Sugano,S.,
Mizuno,K., Narikawa,R., Niikura,J., Oka,M., Ryu,R., Sugano,S.,
Sugiyama,A., Suzuki,Y., Tsunoda,Y., Ueda,M., Xie,Q., Yokomizo,S.,
Yoshimura,A., Matsubara,K. and Murakami,K.
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Submitted (05-DEC-2001) Shoshi Kikuchi, National Institute of
Submitted (05-DEC-2001) Shoshi Kikuchi, National Institute of
Agrobiological Sciences, Department of Molecular Genetics, Head of
Laboratory of Gene Expression; 2-1-2 Kannondai, Tsukuba, Ibaraki
305-8602, Japan (E-mail:skikuchi@nias.affrc.go.jp,
Tel:81-29-838-7007)
Tel:81-29-838-7007, Pax:81-29-838-7007
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Fujimura,T., Fukuda,S., Hanagaki,T., Hara,A., Hashizume,W.,
Hayashida,K., Hayashizaki,Y., Hayatsu,N., Hiramoto,K., Hiraoka,T.,
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Yasunishi,A. and Hayashizaki,Y.
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                                                                                                                                                                                                                                                                                                                                          SerIleSerArgAsnPheValIleSerArgThrProThrGlnValAlaSerHisAlaGln
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                          GCCCAGGTGAAGATCGAGGCCGGCAATTCGCACGTCGCCGGCGGCGGCCGCCTCGACGAC 1292
                                                                            CCTCCGCCGCCGCCGCCGCCGCGCGCGCGCCACCACCACTCATGCCCCATCCCTAC
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                                                 AlaGlyHisMetValProAla-AlaValGlyThrProValValPheProProGlyHisAl
                                                                                                     ProProProMetProMetTyrSerAlaAlaPro---
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Glycine max
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Cloning of soybean genes induced caused by syringolide elicitor planta 218 (4), 606-614 (2004)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; cosids; eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae;
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Glycine max
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                                                                                                                                                                                             /codon_start=1
/product="syringolide-induced protein 1-3-1A"
/protein id="BAB86892.1"
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                                                                                                                                                                                                                                                                                                                                binding factor
                                                                                                                                                                                                                                                                                                                                                                                                                               syringolide"
                                                                                                                                                                                                                                                                                                                                                                                                                                             /cell_type="suspension cultured
/clone_lib="lambda syr-Harosoy"
/note="cDNA_library constructed
                                                                                                                                                                                  DOMGTFGYSNYGFDM"
                                                                                                                                                                                                                                                                                                                                                                               /gene="1-3-1A"
155. .856
                                                                                                                                                                                                                                                                                                                              note="similar to Arabidopsis thaliana inding factor protein"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              clone="1-3-1-3"
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TrpThrArgGluAspAspLysAlaPheGluAsnAlaLeuAlaAlaCysAlaAlaProPro

776 CAGTCACAGCAATACCCATCAAGCAACATG 805
ACTTGGGTTCCTCCT
236 AlaLeuGlyProProGlyMetLysHisHisHisHisHisHisProGlyGlyAlaProPro
716AACTCAGCGCTATG
216 AlaAlaGlnGlnGlyAlaProIleThrGlyHisGlnAlaThrGlyAsnProAlaAlaAla
668 AAAGAGAGAGAGATCAAGCATTCATGACATAACGACTGTGGACAGT
196 ArgAspArgArgSerSerIleHisAspIleThrSerValT
608 ACACCAACTCAAGTAGCCATGCCCAGAATACTTTCTTCGCCAGAATTCGGTGAAG
176 ThrProThrGlnValAlaSerHisAlaGlnLysTyrPheIleA
548 CTTAGTAAGTTTGGGAAGGGAGATTGGAGAAGCATTTCAAGAAJ
156 LeuAspLysPheGlyLysGlyAspTrpArgSerIleSerArgAsnPheVallleSerArg
488 AACGAAAGGAAGGGCACGCCTTGGACTGAAGAGGAACACAGGCTGTTTCTCATTGGG
136 GlnGluArgArgLysGlyIleProTrpThrGluGluGluHisA
455 TCATTCGGTTCCAAGCTTAAACAACAAGGCGAG
116 AspGluArgLysGlyGlyGlyGlyTyrAspGlyGlyLysSerCysSerLysAlaGlu
401 ATGCCGCCCAGTGGCGGTGCTGGAATTTCTACGTGGGACAACGCTAATCAGATC
96 AlaProProAspGlyAlaGlyAlaAlaAlaAlaAlaSerLysA
341 GTCTTCGAGATCGACTCCGGCCGAGTCGAGGTCCCGAGTTACGTCGATGACTCGGTGGCG
76 ValAlaAlaIleAspAlaGlyArgValProLeuProArgTyrA
284 GTTCCCGGCAAGTCGGCGGTGGAGGTAAGGGAACACTACGAGGCCCTCGTCCACGAC
56 ValProGlyAlaArgSerAlaGluGluValArgArgHisTyrG
239
38 ProAlaAspGlyGlyAlaProAspAspAspTrpPheA

Search completed: July 30, 2005, 00:26:00 Job time: 5168 secs

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Result
No.
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-Q2/Cgn2 1/USPTO spool/US10630636/runat 27072005 123226 12158/app query.fasta_1.455
-Q2/Cgn2 1/USPTO spool/US10630636/runat 27072005 123226 12158/app query.fasta_1.455
-DB=N Geneseq_16Dec04 -QFMT=fastap -SUFFIX=rng -MINMATCH=0.1 -LOOPCL=0
-LOOPEXT=0 -UNITS=bite sCTART=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi
-LIST=45 -DOCALIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=15
-MODE=LOCAL -OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000
-USER=US10630636_GCGN_1 1.644 @runat 27072005 123226 12158 -NCPU=6 -ICPU=3
-NO MMAP -LARGEGUERY -NEG SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7
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Abk65370 Arabidops
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Pred. No.:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CC The invention relates to a pure polypeptide comprising a fully defined CC Myb protein transcription factor OBMYBS1, OSMYBS2 or OBMYBS3 protein CC sequence, where the polypeptide regulates expression of a gene in a cell. CC The polypeptide is useful for regulating expression of a gene in a plant cell, preferably rice or barley cell. The method is useful for cell, preferably rice or barley cell. The method is useful for antibody to the polypeptide is useful for detecting the polypeptide. An CC distribution of OSMYBS proteins in tissues and in cellular compartments cc and for verifying the expression of OSMYBS proteins in a transgenic plant. Nucleic acid encoding the polypeptide is useful for generating a cryptessed in a tissue or cell. Nucleic acid encoding the polypeptide is cellular compartment in CC expressed in a tissue or cell. Nucleic acid encoding the polypeptide is cellular compound in a compound consecution of osmyBS many is composed in a condition of cellular compound consecution of a gene regulated by the methods, or as labelled condition of a gene regulated by the polypeptide, e.g. alpha-amylase composed the regulated by the polypeptide, e.g. alpha-amylase componed consecution of a gene regulated by the polypeptide, e.g. alpha-amylase componed consecution of a gene regulated by the polypeptide, e.g. alpha-amylase componed consecution of a gene regulated by the polypeptide, e.g. alpha-amylase componed consecution of a gene regulated by the polypeptide is componed consecution of a gene regulated by the polypeptide is componed consecution of a gene regulated by the polypeptide is componed consecution of a gene regulated by the polypeptide is componed consecution of a gene regulated by the polypeptide is componed consecution of a gene regulated by the polypeptide is componed consecution of a gene regulated by the golypeptide is componed consecution of a gene regulated by the golypeptide is componed consecution of a gene regulated by the golypeptide is componed consecution of a gene regulated by the gol
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          Novel Myb proteins derived from Oryza sativa and designated OsMYBS1, OsMYBS2 or OsMYBS3, useful for regulating expression of a gene in plant cell, preferably rice or barley cell.
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P-PSDB; ADO00783.
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Claim 18;

OBS

ID NO

1; 22pp;

English.

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CC Myb protein transcription factor OsMYBS1, OsMYBS2 or OsMYBS3 protein
CC sequence, where the polypeptide regulates expression of a gene in a cell.
CC The polypeptide is useful for regulating expression of a gene in a plant
CC cell, preferably rice or barley cell. The method is useful for
CC identifying a compound that modulates the activity of the polypeptide. An
CC antibody to the polypeptide is useful for detecting the presence and
CC distribution of OsMYBS proteins in tissues and in cellular compartments
CC and for verifying the expression of OsMYBS proteins in a transgenic
CC plant. Nucleic acid encoding the polypeptide is useful for generating a
CC transgenic plant or producing to determine whether an OsMYBS mRNA is
CC expressed in a tissue or cell. Nucleic acid encoding the polypeptide is
CC also useful as primers in PCR-based detection methods, or as labelled
CC probes in nucleic acid blots (e.g. Northern blots). The compound
CC identified by the method is useful for enhancing or repressing the
CC expression of a gene regulated by the polypeptide, e.g. alpha-amylase
CC comyrBS1.
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                       AlaSerHisAlaGlnLysTyrPheIleArgLeuAsnSerMetAsnArgAspArgArgArg
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GGGATGTATGGTGGGGCCAGTGGGACAACCGATCATCGCACCACCTGATCATATG---
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       ---MetTyrSerAlaAlaProMetGlyHisProValAlaGly------HisMetVal
                                                                                               GGAGGACAACAACCGCAAGTGGTTAAACATAGACCAGCTCAGCCACAACCACAACCACAA
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                                                                                                                         Novel transgenic plant having recombinant polynucleotide encoding polypeptide that alters trait of transgenic plant when compared w trait of another plant lacking recombinant polynucleotide.
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PINEDA O.
HEARD J.
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ADAM L.
BROUN P.
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The invention relates to a transgenic plant having recombinant polynucleotide (II) encoding polypeptide comprising at least 6 consecutive amino acids of a sequence chosen from the protein sequence appearing as ADC46603 - ADC46749 (every second sequence), where recombinant polynucleotide alters a trait of the seed transgenic plant when compared with same trait of another plant lacking recombinant polynucleotide. The proteins are transcription factor-like proteins. Also included are altering (M1) a trait associated with seed (comprising: transforming a plant with (II); selecting the transformed plants; and identifying a transformed plant with seed having altering the proteins are transformed plant (involving transforming the plant with least one gene of a plant (involving transforming the plant with (II) and selecting the transformed plant), altering (M3) a trait associated with a plant's seed (comprising:

Disclosure;

SEQ ID NO

35;

165pp; English.

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US-10-630-636-7 (1-306) x ADC46636
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                sequence, comparing the database sequence with a polypeptide or a polynucleotide chosen as detailed above, selecting a database sequence
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                                                           TATTTCATTCGTCTAAATTCAATGAACAAAGACAGAAGGCGATCAAGCATTCACGACATC
                                                                                        TyrPheIleArgLeuAsnSerMetAsnArgAspArgArgArgSerSerIleHisAspIle
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ThrSerValThrAlaGlyAspGlnValAlaAlaGlnGlnGlyAlaProIleThrGlyHis
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New recombinant polynucleotide for altering the regulation of gene expression of plants to modify the plant's traits, particularly the plant's environmental stress tolerance.

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RESULT 5
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(YUGG/)
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                                                                                                                                                                                                                                                                                                                     Arabidopsis thaliana.
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22-MAR-2000;
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                                                                                                                                                                                                                                                                                                                                                heavy metal; low light;
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                                                                       R, Heard J, Jiang (Keddie J, Ratcliffe
                                                                                                                    KEDDIE J.
RATCLIFFE
PILGRIM M.
ADAM L.
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JIANG C.
PINEDA O.
REUBER L.
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ZHANG
                                            ADD55830
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ThrSerValThrAlaGlyAspGlnValAlaAlaGlnGlyAlaProIleThrGlyHis
                                                                                                                                   IleSerArgAsnPheValIleSerArgThrProThrGlnValAlaSerHisAlaGlnLys
                                                                                                                                                                               GATGAGCACAGGTTATTTCTTCTTGGTTTGGATAAGTACGGGAAAGGTGATTGGCGTAGC
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                                                  TATTTCATTCGTCTAAATTCAATGAACAAAGACAGAAGGCGATCAAGCATTCACGACATC
                                                                   TyrPheIleArgLeuAsnSerMetAsnArgAspArgArgArgSerSerIleHisAspIle
                                                                                                                 ATTTCTCGCAACTTTGTAGTAACAAGAACACCGACCCAAGTTGCGAGCCATGCTCAAAAG
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PR 22-P
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PR 15-J
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                                                                          Keddie J,
Pineda O,
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22-FEB-1999;
11-MAR-1999;
15-APR-1999;
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(REUB/)
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(HEAR/)
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17-FEB-2000;
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15-JUL-1999
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                                                           Creelman
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BROUN P.
PINEDA O.
REUBER L.
ZHANG J.
YU G.
JIANG C.
SAMAHA R.
PILGRIM M.
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HEARD J.
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                                                                            Fromm M,
Reuber L,
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C, Samaha R,
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P-PSDB; ADI61459 WPI; 2004-052052/05

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Best Local Similarity:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The present invention relates to the isolation of novel pla-
(arabidopsis thaliana) polynucleotide sequences that encode
factors (TFs), and the polypeptide sequences for the TFs. T
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TyrPheIleArgLeuAsnSerMetAsnArgAspArgArgArgSerSerIleHisAspIle
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                                                                        ATTTCTCGCAACTTTGTAGTAACAAGAACACCGACCCAAGTTGCGAGCCATGCTCAAAAG
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17-FEB-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  abiotic stress; cold tolerance; heat tolerance; drought; osmotic phosphate limitation; potassium limitation; nitrogen limitation; hormone sensitivity; disease resistance; sugar sensing; seed ger
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2000US-00533029.
2000US-005333029.
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2000US-00533392.
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2000US-00533648.
2000US-00819144.
2001US-00819144.
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2001US-00819146.
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(ZHAN/)

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Conscillation in transcer to a transperit plant comprises a recombinant comprising a sequence encoding a polymelted that initiates can transcription (i.e. a transcription factor) from Arabidopsis, Soybean, comprising any of the sequence appearing as AD001588 changes or Corn, comprising any of the sequences appearing as AD001588 changes are progeny plant, an expression cassette (comprising a progeny plant, an expression cassette (comprising a polymucleotide described above), a host cell comprising the expression cassette, producing a modified plant having a modified trait, identifying cassette, producing a modified plant having a modified trait, identifying cassette, producing a modified plant having a modified trait, identifying cassette, producing a modified plant having a modified trait, identifying cassette, producing a modified trait as subject to a regulatory effect of any of the polymucleotide sequence that is subject to a regulatory effect of any of the polymucleotide sequence that is subject to a regulatory effect of any of the polymucleotide sequence to the polymucleotide described above. The crait e.g. an enhanced tolerance to abiotic stress increased tolerance to heat, tolerance to phosphate limitation, tolerance to potassium cassettion, permination in cold conditions, freezing tolerance, tolerance to betryits, altered susceptibility to mean litered susceptibility to second a stered branching pattern, reduced conditions, altered stem morphology, increased root stem bifurcations, altered show morphology, increased cold caltered leaf development, altered stem morphology, increased cold caltered leaf development, increased leaf size and mass, glossy leaves, caltered seed shape, change in seed shape, change in second morphology, altered seed coloration,
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Pineda O, I
Pilgrim ML,
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improved characteristics
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(CREE/)
(DUBE/)
(RATC/)
(KUMI/)
leaf cell expansion, change in seed morphology, altered seed colorat
increased seed size, decreased seed size, altered seed shape, change
leaf biochemistry, increased leaf wax, an alteration in leaf premyl
content, increased leaf insoluble sugars, decreased leaf insoluble
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SAMAHA R S.
PILGRIM M L.
CREELMAN R A.
DUBELL A N.
RATCLIFFE O.
KUMIMOTO R.
SHERMAN B K.
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PINEDA O.
REUBER T L.
KEDDIE J S.
YU G.
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FROMM
HEARD
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ADAM L J.
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Reuber TL,
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, Keddie JS, Yu
n RA, Dubell AN,
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S, Yu G, Jiang C,
ll AN, Ratcliffe O,
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Samaha RS;
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Query Match:
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LeuGlyProProGlyMetLysHisHisHisHisHisHisProGlyGlyAlaProProPro
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                                                                                                                                                            TyrPheIleArgLeuAsnSerMetAsnArgAspArgArgSerSerIleHisAspIle
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                                AACAACAGCAATÁÁCAACAACAACAACAACAACAACAACAGTTCTCCTGCTGTTGCTGGA
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                                                                                                                     ThrSerValThrAlaGlyAspGlnValAlaAlaGlnGlnGlyAlaProIleThrGlyHis
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CATTACGAGCTTTTAGTTGAAGATGTTACTAGGATTGAATCAGGATGTGTGCCTCCTT
                                                                                                 ACTAGTGTTGGCAACGCAGATGTCTCAACCGCCACAAGG---
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57.64%
48.41%
38.06%
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Indels:
Gaps:
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Conservative:
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encoding an Arabidopsis thaliana transcription factor, their variants, complements, fragments, or related polynucleotide with 31% to 95% sequence identity, where the plant possesses an altered trait as compared to a wild-type or reference plant, or the plant exhibits an altered phenotype as compared to a wild-type or reference plant, or the plant exhibits ectopic expression or altered expression of one or more genes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ABK65275 standard;
                                                                                                                         The invention relates to 1 of 232 isolated or recombinant polynucleotides
                                                                                                                                                                                                                                                                                                                                                                                                                                                (ADAM/)
(RATC/)
(REUB/)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       22-AUG-2000;
16-NOV-2000;
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                                                                                                                                                                Claim 4;
                                                                                                                                                                                                                         An isolated or recombinant polynucleotide used to produce a transgenic
                                                                                                                                                                                                                                                                  P-PSDB;
                                                                                                                                                                                                                                                                                                                             Adam
                                                                                                                                                                                                                                                                                                                                                Pilgrim
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (KEDD)
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DB; AAU93089.
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JIANG C.
                                                                                                                                                                                                                                                                                                                                                Ξ,
                                                                                                                                                                                                                                                                                                                                                                                                            YU G.
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                                                                                                                                                                                                                                                                                                                                                                                       PINEDA O.
                                                                                                                                                                                                                                                                                                                                                                                                                               RIECHMANN J
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CREELMAN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ADAM L.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TIBELL
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    Creelman
Ratcliff O,

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                                                                                                                                                                Page 527-528;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        chemical;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           gene; transcription factor; transgenic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   cDNA encoding a transcription factor #127
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2000US-00713994.
2001US-00837944.
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                                                                                                                                                                                                                                                                                                                         R, Dubell AJ, Heard J, Reuber JL, Riechmann JL,
                                                                                                                                                            941pp;
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                                                                                                                                                                                                                                                                                                                         Jiang C,
L, Yu G,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           agriculture;
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                                                                                                                                                                                                                                                                                                                             Pineda
                                                                                                                                                                                                                                                                                                                         Keddie J;
Pineda O;
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457.50
58.02%
42.39%
27.88%
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CC associated with a plant trait as compared to a wild plant. Also included CC are a transgenic plant comprising the polynucleotides, a computer CC readable medium having stored sequence information, and identifying a CC homologue sequence from a database comprising a plurality of known plant CC sequences comprising inputting sequence information selected from one of CC 464 fully defined sequences given in the specification. The isolated or CC recombinant polynucleotide is used for producing a plant having a CC modified trait, the method comprising selecting a polynucleotide that CC encodes a polypeptide or an antisense nucleic acid, inserting the CC polynucleotide or antisense nucleic acid, inserting the CC introducing the vector into a plant or a cell of a plant to overexpress CC the polypeptide or antisense nucleic acid, thereby producing a modified CC plant, and selecting for a modified trait (e.g. increased production of CC environmental stress response (e.g. drought), microbial disease conditions of metabolic chemicals, pest tolerance, resistance, herbicide resistance, seed and fruit yield, growth rate, leaf and flower senescence and many other traits listed in the specification). present sequence is one of the 232 polynucleotides liana transcription factor encoding an

G; 184 Η, 0 Ġ; 0 Other;

Gaps: Mismatches: Indels: Conservative: Matches: Length: 9 47

(1-867)

206	TyrPheIleArgLeuAsnSerMetAsnArgAspArgArgArgSerSerIleHisAspIle 206	187	Ş
555		496	В
186	IleSerArgAsnPheVallleSerArgThrProThrGlnValAlaSerHisAlaGlnLys	167	8
495		436	Дb
166	GluGluHisArgLeuPheLeuLeuGlyLeuAspLysPheGlyLysGlyAspTrpArgSer	147	Ş
435	CGGTCGCAGGCCGGTAGATCGCCGGAGCTGGAGCGGAAGAAAGGCGTTCCTTGGACGGAG	376	В
146	AlaGluGlnGluArgArgLysGlyIleProTrpThrGlu :	134	Ş
375		322	Dр
133	ArgLysGlyGlyGlyGlyTyrAspGlyGlyLysSerCysSerLys	118	δ
321	CTAGATTGGGCC	310	Ъ
117	AspGlyAlaGlyAlaAlaAlaAlaAlaSerLysAspGlyGlyHisArgArgAspGlu 117	99	Ş
309	GCCGGTTTAATCCCGGTCCCCCGGTTACATCACCTCGCCGCCTTTCACT	262	рь
86	AlaGlyArgValProLeuProArgTyrAlaGlyGluGluSerAlaAlaProPro	81	Ş
261		202	Б
80	SerAlaGluGluValArgArgHisTyrGluAlaLeuValGluAspValAlaAlaIleAsp	61	Ş
201		151	Дb
60		41	Ş
150	GCAGAGAACAAGGCATTCGAGAATGCTTTGGCGGTTTACGAC	109	дb
40	GluAspAspLysAlaPheGluAsnAlaLeuAlaAlaCysAlaAlaProProProAlaAsp	21	Ş
108	CTCATGGAGGAAACTAAGAGCGGCGTCGCAGCTTCTGGTGAAGGTGCCACGTGGACGGCG	49	D D
20	MetThrSerGlnAlaAlaThrThrThrThrThrAlaAlaAlaAlaAlaAlaTrpThrArg	1	ş

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Percent Similarity:
Best Local Similarity:
                                       Alignment Scores:
Pred. No.:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    19-NOV-2001;
11-DEC-2001;
14-JUN-2002;
                                                                                               transcription factor polymucleotides and polypeptides are useful in producing transgenic plants with commercially valuable properties, i.e. modified or altered desirable traits as compared to a reference plant, such as an alteration in a plant growth characteristic, e.g. growth rate, germination rate of seeds, vigor of plants and seedlings, or leaf and flower senescence. Sequence information related to the polynucleotides and polypeptides can also be used in bioinformatic search methods. The transgenic plant is useful for growing a progeny plant from a parent plant. This sequence represents one of the cDNAs of the invention.
                                                                                                                                                                                                                                                                                                    New plant transcription factor polynucleotides and polypeptides, useful in producing transgenic plants with commercially valuable properties, such as an alteration in a plant growth characteristic, e.g. growth rate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        09-AUG-2001;
                                                                          Sequence 867
                                                                                                                                                                                                            The invention relates to a number of isolated Arabidopsis thaliana cDNA sequences and their encoded proteins which are especially transcription factor related cDNA's and proteins. The isolated or recombinant plant
                                                                                                                                                                                                                                                                 Disclosure; SEQ ID NO
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                                                                                                                                                                                                                                                                                                                                                        P-PSDB;
                                                                                                                                                                                                                                                                                                                                                                                                                   Ratcliffe O,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  09-AUG-2002; 2002WO-US025805
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WO2003013227-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Arabidopsis thaliana.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Plant yield-related polynucleotide clone G1641.
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                                                                                                                                                                                                                                                                                                                                                                                                                                             (MEND-) MENDEL BIOTECHNOLOGY INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               transcription factor; transgenic plant; growth rate; senescence;
                                                                                                                                                                                                                                                                                                                                                                  2003-248221/24.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   germination rate;
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; 2001US-0336049P.
; 2001US-0338692P.
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Jiang C, Reub
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                                                ds; gene; transcription factor; transgenic plant; salt stress resistance;
osmotic stress resistance; freezing tolerance; drought tolerance;
              Arabidopsis thaliana
                                                                                    Plant yield related polynucleotide clone G1641.
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                                     osmotic stress
low humidity to
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                                       tolerance; radiation
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19-NOV-2001;
11-DEC-2001;
14-JUN-2002;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The invention relates to a number of isolated cDNA sequences and their encoded proteins which are especially transcription factor related cDNA's and proteins. The isolated or recombinant plant transcription factor polymucleotides and polypeptides are useful in producing transgenic plants with commercially valuable properties, i.e. modified or altered desirable traits as compared to a reference plant, e.g. salt stress resistance, osmotic stress resistance, tolerance to freezing, drought, low humidity tolerance, or radiation resistance. Sequence information related to the polymucleotides and polypeptides can also be used in bioinformatic search methods. The transgenic plant is useful for growing a progeny plant from a parent plant. This sequence represents one of the cDNAs of the invention
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AlaGlyArgValProLeuProArgTyrAlaGlyGluGluSerAlaAlaProPro-----
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Jiang C,
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; 2001US-0336049P.
; 2001US-0338692P.
; 2002US-00171468.
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1. .867
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/product= "transcription factor"
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Ratcliffe O,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              transgenic; plant; enhanced tolerance to abiotic stress;
(HEAR/)
(HAAK/)
(CREE/)
(RATC/)
(ADAM/)
                                                                                            (SHER/)
(RIEC/)
(JIAN/)
                                                                                                                                                                                                                                                   29-JAN-2004.
                                                                                                                                                                                                                                                                                                                           Unidentified
                                                                                                                                                                                                                                                                                                                                                               transcription
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                                   RIECHMANN J L.
) JIANG C.
) HEARD J E.
) HAAKE V.
) CREELMAN R A.
RATCLIFFE O. ADAM L J.
                                                                                                                                     SHERMAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     standard;
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Query
DB:
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Pred. No.:
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                                                                                                                                                                                                                                                                                                                           Percent Similarity:
Best Local Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                         The invention describes a transgenic plant comprising a recombinant CC polynucleotide of any one of more than 500 nucleotide sequences fully CC defined in the specification or its complement. The method of the CC invention can be used to produced a plant having altered traits such as: CC enhanced tolerance to abiotic stress; glyphosphate tolerance; hormone CC sensitivity; disease resistance; sugar sensing; early or late flowering; CC entered flower structure, change in stem bifurcations, altered branching pattern, reduced apical dominance, reduced trichome density; lack of trichome; reduced apical dominance, reduced trichome density; lack of trichome; reduced ectopic trichome number; altered stem morphology; cincreased root growth; increased root hairs; altered seed development; correlated increased neotosis; increase in trichome number; altered seed development; correlature sensescence, increased neotosis; increase in seedling or plant correlature sensescence, increased neotosis; increase in seedling or plant size; decreased plant size; leaf morphology; seed morphology; seed sichemistry; increase in root anthocyanins; increase in plant correlated plant, polynucleotides and polypeptides are useful in transgenic plant, polynucleotides and polypeptides are useful in transgenic plant, related polynucleotides and polypeptides are useful in transgenic plant, related polynucleotides. This sequence represents a plant
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(KEDD/)
(BROU/)
(PILG/)
(DUBE/)
(PINE/)
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DB; ADI44217.
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KEDDIE J.

BROUN P E.

PILGRIM M L.

DUBELL A N.

PINEDA O.

YU G.
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            GCCGGTTTAATCCCGGTCCCCGGTTACATC------ACCTCGCCCCTTTCACT
                                   AlaGlyArgValProLeuProArgTyrAlaGlyGluGluSerAlaAlaProPro-----
                                                                                    SerAlaGluGluValArgArgHisTyrGluAlaLeuValGluAspValAlaAlaIleAsp
                                                                                                                 GACAACACTCCTGATCGG-----TGGCAGAAGGTGGCTGCGGTGATTCCGGGG---AAG
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, Ratcliffe (
Dubell AN,
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457.50
58.02%
42.39%
27.88%
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O, Adam LJ,
Pineda O, Yu
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Matches:
Conservative:
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Reuber TL,
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Keddie
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16-NOV-2000;
18-APR-2001;
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metabolic c
microbial d
                                   (KBDD/)
(ADAM/)
(RATC/)
(REUB/)
(RIEC/)
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(PILG/)
(CREE/)
(DUBE/)
                                                                                                   (HEAR/)
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                                                                                                                                                                                                                                                                                                                             Arabidopsis thaliana.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ABK65273;
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                                                                                                                                                                                                                                                                                                                                                      fruit yield; growth rate; leaf senescence; flower senescence.
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                                                                                    CREELMAN R.
DUBELL A J.
HEARD J.
JIANG C.
KEDDIE J.
                                   RATCLIFF O.
REUBER J L.
RIECHMANN J L.
                         S
             PINEDA
                                                                         ADAM L.
                                                                                                                                                                  MENDEL BIOTECHNOLOGY INC.
                                                                                                                                                        PILGRIM M.
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                                                                                                                                                                                                                                                                                                                                                                  ; gene; transcription factor; transgenic; agriculture;
chemical; environmental stress; drought;
disease resistance; herbicide resistance; seed yield;
                                                                                                                                                                                            2000US-0227439P.
2000US-00713994.
2001US-00837944.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GC 464 fully defined sequences given in the specification. The isolated or crecombinant polynucleotide is used for producing a plant having a CC modified trait, the method comprising selecting a plant having a CC modified trait, the method comprising selecting a polynucleotide that CC modified trait, the method comprising selecting a polynucleotide that CC polynucleotide or antisense nucleic acid into an expression vector, introducing the vector into a plant or a cell of a plant to overexpress CC the polypeptide or antisense nucleic acid, thereby producing a modified CC plant, and selecting for a modified trait (e.g. increased production of agriculturally useful proteins or metabolic chemicals, pest tolerance, CC environmental stress response (e.g. drought), microbial disease CC resistance, herbicide resistance, seed and fruit yield, growth rate, leaf CC and flower senescence and many other traits listed in the specification). The present sequence is one of the 232 polynucleotides encoding an A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              encoding an Arabidopsis thaliana transcription factor, their variants, complements, fragments, or related polynucleotide with 31% to 95% sequence identity, where the plant possesses an altered trait as compared to a wild-type or reference plant, or the plant exhibits an altered phenotype as compared to a wild-type or reference plant, or the plant exhibits ectopic expression or altered expression of one or more genes associated with a plant trait as compared to a wild plant. Also included
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Pilgrim
Adam L,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        are a transgenic plant comprising the polynucleotides, a computer readable medium having stored sequence information, and identifying
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Ratcliff O,
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19-NOV-2001;
11-DEC-2001;
14-JUN-2002;
                                                                                                                                                                                                                         New plant transcription factor polymucleotides and polypeptides, usef in producing transgenic plants with commercially valuable properties, such as an alteration in a plant growth characteristic, e.g. growth r
                                                                                                                                                                                                                                                                                                                                                                                                          Ratcliffe O,
Pilgrim ML,
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The invention relates to a number of isolated Arabidopsis thaliana cDNA sequences and their encoded proteins which are especially transcription factor related cDNA's and proteins. The isolated or recombinant plant transcription factor polynucleotides and polypeptides are useful in producing transgenic plants with commercially valuable properties, i.e. modified or altered desirable traits as compared to a reference plant,

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RESULT 14
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               ADI44214;
                                       ADI44214 standard; DNA;
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                                                                                            GGGAGTCCTGTTCAGGCGCCGCAG
                                                                                                                                             ACTACGGTTGATGCTACTTTGGCTATGCCTGGGTCTAACATGGACTGGACTGGCCAACAC
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Matches:
Conservative:
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The invention describes a transgenic plant comprising a recombinant CC polynucleotide of any one of more than 500 nucleotide sequences fully CC defined in the specification or its complement. The method of the CC invention can be used to produced a plant having altered traits such as: enhanced tolerance to abiotic stress; glyphosphate tolerance; hormone CC enhanced tolerance to abiotic stress; glyphosphate tolerance; hormone CC enhanced troity; disease resistance; sugar sensing; early or late flowering; CC altered flower structure, change in stem bifurcations, altered branching CC pattern, reduced apical dominance, reduced trichome density; lack of CC trichomes; reduced ectopic trichome development; altered trichome CC development; increase in trichome number; altered seed development; CC increased root growth; increased root hairs; altered seed development; CC altered cell proliferation or cell differentiation; rapid development; CC premature sensescence; increased neorphology; seed morphology; seed correased plant size; leaf morphology; seed morphology; seed correased plant size; leaf morphology; seed morphology; seed correase in plant cc anthocyanins, or alteration in light response or shade avoidance. The corresponse or shade avoidance corresponse or shade avoidance. The corresponse or shade avoidance.

Disclosure; methods.

SEQ ID

NO 2677; 435pp; English.

New transgenic plant comprising a recombinant of more than 500 nucleotide sequences, useful

polynucleotide of any in bioinformatic searc

search

P-PSDB;

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(SHER/)
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(CREE/)
                                                                                                                                                                                                                                                                                                                                                                                                                                                           sugar sensing; flowering; flower structure; stem bifurcation; branching pattern; apical dominance; trichome; stem morphology; root growth; root hair; seed development; cell proliferation; cell differentiation; premature senescence; necrosis; plant size; leaf morphology; seed morphology; seed biochemistry; root anthocyanin; plant anthocyanin; light response; shade avoidance; bioinformatic;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                transgenic; plant; enhanced tolerance to abiotic stress;
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DB; ADI44215.
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REUBER T L.
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PILGRIM M L.
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Percent Similarity:
Best Local Similarity:
Query Match:
DB:
 RESULT 15
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 Hybridisation assay; genetic mapping; gene expression control; protein identification; signal transduction pathway; metabolic promoter; termination sequence; ss.
                                            Arabidopsis thaliana DNA fragment SEQ
                                                                   18-OCT-2000
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Matches:
Conservative:
Mismatches:
Indels:
Gaps:
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                                            ID NO: 58335.
                                                                                                                                                                                                                     -GlyAspGlnVal-----AlaAlaGlnGln
           pathway; metabolic pathway;
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Indels:
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621 ACTACGGTTGATGCTACTTTGGCTATGCCTGGGTCTAACATGGACTGGACTGGCCAACAC	밁
207 ThrSerValThrAlaGlyAspGlnValAlaAlaGlnGln 219	8
561 TATTTTCTGAGACAGAACTCGGTGAAGAAGGAGGAGAAGGAAG	뮍
187 TyrPheIleArgLeuAsnSerMetAsnArgAspArgArgArgSerSerIleHisAspIle	Ş
501 ATCTCGAGAAACGTTGTGGTGACGAGGACACCGAGGCAAGTCGCGAGTCACGCTCAGAAG	뭥
167 IleSerArgAsnPheVallleSerArgThrProThrGlnValAlaSerHisAlaGlnLys	Ş
441 AACGAACACAAATTGTTTCTGATCGGATTAAAGAGATATGGTAAGGGAGAGTTGGAGGAGT	뮍
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405GAGAGTGAACGCAAAAGAGGAACTCCTTGGACAGAG	Db
127 GlyGlyLysSerCysSerLysAlaGluGlnGluArgArgLysGlyIleProTrpThrGlu	δ
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Search completed: July 29, 2005, 22:59:56 Job time: 625 secs

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Result
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Listing first 45 summaries
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US-09-640-211A-1666
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Sequence 1534, Ap
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Sequence 1820, Ap
Sequence 1420, Ap
Sequence 553, App
Sequence 2058, App
Sequence 2013, Ap
Sequence 2031, Ap
Sequence 2038, App
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1100 7570 1, 7 1, 7	Sequence 2, Appli Sequence 1541, Ap Sequence 740, App Sequence 2, Appli Sequence 1, Appli	787, 787, 2026, 255, 15611	Sequence 1250, Ap Sequence 1250, Ap Sequence 1269, Ap Sequence 1284, Ap Sequence 1366, Ap Sequence 1366, Ap Sequence 1953, Ap Sequence 1953, Ap Sequence 799, App Sequence 799, App Sequence 1301, Ap Sequence 3018, Ap Sequence 1301, Ap Sequence 1301, Ap

## ALIGNMENTS

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RESULT 1

US-09-640-211A-1534/c

US-09-640-211A-1534/c

Sequence 1534, Application US/09640211A

Patent No. 6833446

GENERAL INFORMATION:
APPLICANT: Wood, Marion
APPLICANT: Wood, Marion
APPLICANT: Shenk, Michael A.
APPLICANT: Glenn, Matthew
TITLE OF INVENTION: Compositions and Methods for the
TITLE OF INVENTION: Modification of Gene Transcription
FILE REFERENCE: 11000.1021C1U

CURRENT FILING DATE: 2000-08-16

NUMBER OF SEQ ID NOS: 2368
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 1534
LENGTH: 574
TYPE: DNA
ORGANISM: Eucalyptus grandis
US-09-640-211A-1534

Alignment Scores:
Score:
Pred. No.:
SCOTE: 3.31e-25
Best Local Similarity: 57.88*
Descrent Similarity: 57.88*
Ouery Match: 25
DB:
US-10-630-636-7 (1-306) x US-09-640-211A-1534 (1-574)
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; LENGTH: 335
; TYPE: DNA
; ORGANISM: Eucalyptus grandis
; PEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)...(335)
; OTHER INFORMATION: n = A,T,C o
US-09-640-211A-1484
                                                                                                                                                                                                                                                                                                                                                                                                                                    GENERAL INFORMATION:

APPLICANT: Wood, Marion
APPLICANT: Shenk, Michael A.
APPLICANT: Shenk, Michael A.
APPLICANT: Shenk, Michael A.
APPLICANT: Shenk, Matchew
TITLE OF INVENTION: Compositions and Methods for the
TITLE OF INVENTION: Modification of Gene Transcription
FILE REFERENCE: 11000.1021CIU
CURRENT APPLICATION NUMBER: US/09/640,211A
CURRENT FILING DATE: 2000-08-16
NUMBER OF SEG ID NOS: 2368
SOFTWARE: FastSEQ for Windows Version 4.0
SEG ID NO 1484
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132 SerLysAlaGluGluArgArgLysGlyIleProTrpThrGluGluGluHis-----
                                                                  116 AspGluArgLysGlyGlyGlyGlyGly------TyrAspGlyGlyLysSerCys 131
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       114 ArgArgAspGluArgLysGlyGlyGlyGlyGlyTyrAsp-------GlyGlyLysSer 130
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                                       TTATTTCTTCTAGGCCTAGATAAATATGGGAAAGGCGATTGGCGAAGTATTTCCCCGGAAC
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Db Qy	B &	B	US-10-630 Qy Db	Alignment Pred. No. Score: Percent S: Best Loca Query Matt	RESULT 3 US-09-640-211A Sequence 182 Patent No. 6 GENERAL INFC APPLICANT: APPLICANTT: APPLICANTT: APPLICANTT:	Db Qy	Db Qy	D Qy	D Qy	Db
143 oTrpThrGluGluGluHisArgLeuPheLeuLeuGlyLeuAspLysPheGlyLysGlyAs 163	GlyTyrAspGlyGlyLys-SerCysSerLysAlaGluGlnGluArgArgLysGlyIlePr    ::: 	84 ValProLeuProArgTyrAlaGlyGluGluSerAlaAlaProProAspGlyAlaGlyAla 103	)-636-7 (1-306) x US-09-640-211A-1824 (1-332) 64 GluValArgArgHisTyrGluAlaLeuValGluAspValAlaAlaIleAspAlaGlyArg 83	gnment Scores:       2.68e-19       Length:       332         d. No.:       2.68e-19       Matches:       72         re:       336.50       Matches:       72         cent Similarity:       71.07%       Conservative:       14         cent Similarity:       59.50%       Mismatches:       23         ry Match:       20.51%       Indels:       13         ry Match:       4       Gaps:       3	SSULT 3 :-09-640-211A-1824 :-09-640-211A-1824 Patent No. 6833446 GENERAL INFORMATION. APPLICANT: Wood, Marion APPLICANT: Wood, Marion APPLICANT: Shenk, Michael A. APPLICANT: McGrath, Annette APPLICANT: McGrath, Annette APPLICANT: McGrath, Matthew TITLE OF INVENTION: Compositions and Methods for the TITLE OF INVENTION: Modification of Gene Transcription FILE REFERENCE: 11000.1021C10 CURRENT APPLICATION NUMBER: US/09/640,211A CURRENT FILING DATE: 2000-08-16 NUMBER OF SEQ ID NOS: 2368 SOFTWARE: FastSEQ for Windows Version 4.0 SEQ ID NO 1824 TYPE: DNA ORGANISM: Finus radiata	204 HisAspIleThrSerValThrAlaGlyAsp 213            :::    304 CATGATATCACTACCGTAGGCAGTGGAGAC 333	184 AlaGlnLysTyrPheIleArgLeuAsnSerMetAsnArgAspArgArgArgSerSerIle 203	164 TrpArgSerIleSerArgAsnPheVallleSerArgThrProThrGlnValAlaSerHis 183	150ArgieuPheLeuLeuGlyLeuAspLysPheGlyLysGlyAsp 163	::::::::

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422 69 117 18 13

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237 217 197 120 177

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APPLICANT: Wood, Marion
APPLICANT: Shenk, Michael A.
APPLICANT: Shenk, Michael A.
APPLICANT: Glenn, Matthew
TITLE OF INVENTION: Compositions and Methods for the
TITLE OF INVENTION: Modification of Gene Transcription
FILE REFERENCE: 11000.1022C1U
CURRENT APPLICATION NUMBER: US/09/640,211A
CURRENT FILING DATE: 2000-08-16
NUMBER OF SEQ ID NOS: 2368
SOPTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 1420
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Best Local Similarity:
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; TYPE: DNA
; ORGANISM: Eucalyptus
US-09-640-211A-1420
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APPLICANT: Wood, Marion
APPLICANT: Shenk, Michael A.
APPLICANT: Shenk, Michael A.
APPLICANT: Glenn, Matthew
TITLE OF INVENTION: Compositions and Methods for the
TITLE OF INVENTION: Modification of Gene Transcripti
FILE REFERENCE: 11000.1021C1U
CURRENT APPLICATION NUMBER: US/09/640,211A
CURRENT APPLICATION NUMBER: US/09/640,211A
CURRENT FILING DATE: 2368
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APPLICANT: Shenk, Michael A.
APPLICANT: Shenk, Michael A.
APPLICANT: Glenn, Matthew
TITLE OF INVENTION: Compositions and Methods for the
TITLE OF INVENTION: Modification of Gene Transcription
FILE REFERENCE: 11000.1021C1U
CURRENT APPLICATION NUMBER: US/09/640,211A
CURRENT FILING DATE: 2000-08-16
NUMBER OF SEQ ID NOS: 2368
SOFTWARE: FASTSEQ for Windows Version 4.0
SEQ ID NO 553
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; SEQ ID NO 1666
; LENGTH: 422
; TYPE: DNA
; ORGANISM: Pinus ra
                        US-10-630-636-7
                                                                                Query Match:
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                                                                                                                                                                                                                                         TYPE: DNA ORGANISM: Pinus
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                        x US-09-640-211A-553 (1-883)
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US-09-640-211A-2058
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SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 2058
LENGTH: 436
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TITLE OF INVENTION: Compositions and Methods for the TITLE OF INVENTION: Modification of Gene Transcription FILE REFERENCE: 11000.1021C1U CURRENT APPLICATION NUMBER: US/09/640,211A CURRENT FILING DATE: 2000-08-16
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APPLICANT: Shenk, Michael A.
APPLICANT: McGrath, Annette
APPLICANT: Glenn, Matthew
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TYPE: DNA
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                                   182
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 GlnGlyAlaProIle-----ThrGlyHisGlnAlaThrGlyAsnProAlaAlaAlaAla 236
                                                                ArgArgSerSerIleHisAspIleThrSerValThrAlaGlyAspGlnValAlaAlaGln
                                                                                                                                 GlnValAlaSerHisAlaGlnLysTyrPheIleArgLeuAsnSerMetAsnArgAspArg 198
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RESULT
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; ORGANISM: Eucalyptus
US-09-640-211A-2013
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CURRENT APPLICATION NUMBER: US/09/640,211A
CURRENT FILING DATE: 2000-08-16
NUMBER OF SEQ ID NOS: 2368
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 2013
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APPLICANT: McGrath, Annette
APPLICANT: Glenn, Matthew
TITLE OF INVENTION: Compositions and Methods for the
TITLE OF INVENTION: Modification of Gene Transcription
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GlyLysGlyAspTrpArgSerIleSerArgAsnPheVallleSerArgThrProThrGln
                                                                  LysGlyIleProTrpThrGluGluHisArgLeuPheLeuLeuGlyLeuAspLysPhe 159
                                                                                                                                                                                                   GlyAlaGlyAlaAlaAlaAlaAlaSerLysAspGlyGlyHisArgArgAspGluArgLys 119
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                                                                                                                                       GlyGlyGlyGlyTyrAspGlyGlyLysSerCysSerLysAlaGluGlnGluArgArg 139
                                                                                                                                                                     AACCCCGGCTCGTCCCCGATCGACGGGAGCGACGGCTACCTGTCCGACGATCCCGCGCCC
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                                               AAAGGTAACCCATGGACGGAAGAAGACCATCGAAGGTTTTTAATTGGTCTCCAGAAATTG
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GGTAAAGGAGACTGGCGAGGGATAGCTCGTGACTTTGTGACTACAAGGACTCCTACTCAA

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; APPLICANT: Wood, Marion
; APPLICANT: Shenk, Michael A.
; APPLICANT: Shenk, Michael A.
; APPLICANT: Glenn, Matthew
; TITLE OF INVENTION: Compositions and Methods for the
; TITLE OF INVENTION: Modification of Gene Transcription
; FILE REFERENCE: 11000.1021C1U
; CURRENT APPLICATION NUMBER: US/09/640,211A
; CURRENT FILING DATE: 2000-08-16
; NUMBER OF SEQ ID NOS: 2368
; SOFTWARE: FASTSEQ for Windows Version 4.0
; SEQ ID NO 232
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Pred. No.:
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; TYPE: DNA
; ORGANISM: Eucalyptus
US-09-640-211A-232
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                                                                     GCAACAAGGGCCACAACTCCAGGACCTGCCCCGTCCGCG---
                                                                                           AlaLeuAlaAlaSerValProGly---AlaArgSerAlaGluGluValArgArgHisTyr
                                                                                                                                 GCGAGTCCCGACCCCCGGCGCCATGACGCGGCGATGCTCCCACT-----
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Sequence 2038, Application US/09640211A

Patent No. 6833446

GENERAL INFORMATION:

APPLICANT: Wood, Marion
APPLICANT: Shenk, Michael A.
APPLICANT: Shenk, Michael A.
APPLICANT: Glenn, Matthew
TITLE OF INVENTION: Compositions and Methods for the
TITLE OF INVENTION: Modification of Gene Transcription
FILE REFERENCE: 11000.1021C1U
CURRENT APPLICATION NUMBER: US/09/640,211A
CURRENT FILING DATE: 2000-08-16
NUMBER OF SEQ ID NOS: 2368
NUMBER OF SEQ ID NOS: 2368
SOFTWARE: FastSEQ for Windows Version 4.0
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; LENGTH: 599
; TYPE: DNA
; ORGANISM: Eucalyptus
US-09-640-211A-1960
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LENGTH:
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APPLICANT: Wood, Marion
APPLICANT: Shenk, Michael A.
APPLICANT: McGrath, Annette
APPLICANT: Glenn, Matthew
                                                                     NUMBER OF SEQ ID NOS: 2368
SOFTWARE: FastSEQ for Winds
SEQ ID NO 1960
                                                                                                                                                                                                                                                                                                    Sequence 1960, Application US/09640211A Patent No. 6833446
                                                                                                                    TITLE OF INVENTION: Compositions and Methods for the TITLE OF INVENTION: Modification of Gene Transcription FILE REFERENCE: 11000 1021C1U CURRENT APPLICATION NUMBER: US/09/640,211A CURRENT FILING DATE: 2000-08-16
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ORGANISM: Pinus radiata
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APPLICANT: Wood, Marion
APPLICANT: Wood, Marion
APPLICANT: Shenk, Michael A.
APPLICANT: Glenn, Matthew
APPLICANT: Glenn, Matthew
TITLE OF INVENTION: Compositions and Methods for the
TITLE OF INVENTION: Modification of Gene Transcription
FILE REFERENCE: 11000.1021C1U
CURRENT APPLICATION NUMBER: US/09/640,211A
CURRENT FILING DATE: 2000-08-16
NUMBER OF SEQ ID NOS: 2368
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 1984
LENCTH: 332
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US-09-640-211A-1984
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    Percent Similarity:
                                   Pred. No.:
                                                                                US-09-640-211A-1984
                                                                                                                                                                                                                                                                                                                              Sequence 1984, Application Patent No. 6833446 GENERAL INFORMATION:
                                                                                             TYPE: DNA ORGANISM: Pinus radiata
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APPLICANT: McGrath, Annette
APPLICANT: Glenn, Matthew
TITLE OF INVENTION: Compositions and Methods for the
TITLE OF INVENTION: Compositions and Methods for the
TITLE OF INVENTION: Modification of Gene Transcription
FILE REFERENCE: 11000.1021C1U
CURRENT APPLICATION NUMBER: US/09/640,211A
CURRENT FILING DATE: 2000-08-16
NUMBER OF SEQ ID NOS: 2368
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 1955
LENGTH: 470
TYPE: DNA
ORGANISM: Eucalyptus grandis
US-09-640-211A-1955
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 1955, Application Patent No. 6833446
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Wood, Marion
APPLICANT: Shenk, Mich
APPLICANT: McGrath, An
APPLICANT: Glenn, Matt
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          156 LeuAspLysPheGlyLysGlyAspTrpArgSerIleSerArgAsnPheVallleSerArg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             136 GlnGluArgArgLysGlyIleProTrpThrGluGluGluHisArgLeuPheLeuLeuGly
                                                                              128
                                                                                                                                111 GlyGlyHisArgArgAspGluArgLysGlyGlyGlyGlyGlyTyr-----AspGly---
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GlyGluGluSerAlaAlaProProAspGlyAlaGlyAlaAlaAlaAlaAlaSerLysAsp
           GluGluHisArgLeuPheLeuLeuGlyLeuAspLysPheGlyLysGlyAspTrpArgSer
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                                                                                                      ATCGGCGAGAACTCTGATAAA------GCATCCCTCGGCTATCTGTCGGATGGCCTG
                                                                                                                                                          GGTCACGAGTTCACTTCGTCGCCTGCCTCGTCGTCCTCCTCCTCGCGAATCTCC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Shenk, Michael A.
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ORGANISM: Eucalyptus
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US-10-630-636-7 (1-306) x US-09-640-211A-1250 (1-632)
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                          146 GluGluGluHisArgLeuPheLeuLeuGlyLeuAspLysPheGlyLysGlyAspTrpArg 165
                                                                                                                                                                                                                                                                                                                                                                                                              212 GACCCCATGAGGAAGAGCGTGAGCCTGAACAACCTGTCGGAGTACGAGCAGCCCCAGGAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          341 GTTGATGTCAAAACCGCGGCGGGTGATCGTTTAGGCAGTTTGACGGCCAAGCCG
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                                                                                                                                                                                                                                                                                                          ThrSerVal-----ThrAlaGlyAspGlnValAlaAlaGlnGlnGlyAlaPro 222
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GAGGATGAACACCGGCTGTTCCTGCTCGGGCTACAGAAAGTAGGAAAGGGCGATTGGAGA
                                                                                                                                                 AspGlyGlyLysSerCysSerLysAlaGluGlnGluArgArgLysGlyIleProTrpThr 145
                                                                                                                                                                                                       GCGTCCGCCGACGA-AGCCGTCGCGCACGGCTCGAAAGGCGGGCCGGC-------
                                                                                                                                                                                                                                                    AlaSerLysAspGlyGlyHisArg---ArgAspGluArgLysGlyGlyGlyGlyGlyTyr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ACCGCCGCCGGCGCC-----GGGGAGTTCATGCTGTTCGGGGGTCAGGGTGGTGGTGGTG
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GENERAL INFORMATION:

APPLICANT: Wood, Marion
APPLICANT: Mood, Marion
APPLICANT: McGrath, Annette
APPLICANT: McGrath, Annette
APPLICANT: McGrath, Annette
APPLICANT: McGrath, Matthew
ITILE OF INVENTION: Compositions and Methods for the
ITILE OF INVENTION: Modification of Gene Transcription
FILE REFERENCE: 11000.1021C1U
CURRENT APPLICATION NUMBER: US/99/640,211A
CURRENT FILING DATE: 2000-08-16
NUMBER OF SEQ ID NOS: 2368
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQ ID NO 2059
LENGTH: 624
TYPE: DNA
ORGANISM: Pinus radiata
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                                                                                          486
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                                 546
                                                               171
                                                                                                          151 LeuPheLeuLeuGlyLeuAspLysPheGlyLysGlyAspTrpArgSerIleSerArgAsn
                                                                                                                                                   426
                                                                                                                                                                 131 CysSerLysAlaGluGlnGluArgArgLysGlyIleProTrpThrGluGluGluHisArg
                                                                                                                                                                                                                                                                     336 GCTGACCCCTCCGAGCCGGCCTCTGCCGCTGCTGCCGCG------
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 226 HisGlnAlaThrGlyAsnProAlaAlaAlaAlaLeuGlyProProGlyMetLysHisHis 245
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          206 IleThrSerValThrAlaGlyAspGlnValAlaAlaGlnGlnGlyAlaProIleThrGly 225
                                                                                                                                                                                                                                                                                              95 AlaAlaProProAspGlyAlaGlyAlaAlaAlaAlaAlaSerLysAspGlyGlyHisArg 114
   LeuAsnSerMetAsnArg 196
                                              PheVallleSerArgThrProThrGlnValAlaSerHisAlaGlnLysTyrPheIleArg
                                                                                          ATGTTTTTGCTAGGTTTGCAGAAGCTTGGCAAAGGTGATTGGAGAGGGAATAGCACGGAAT
                                                                                                                                                  ACTTCCTCCAATTCTCGCGAGCGGAAGAAGGTGTGCCATGGACAGAGGAACATAGA
                                                                                                                                                                                                                                   ArgAspGluArgLysGlyGlyGlyGlyGlyTyr-----AspGly------GlyLysSer 130
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                                 TTTGTCATAACACGAACACCTACACAGGTAGCCAGCCATGCACAGAAATATTTTATTCGA
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294.00
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17.92%
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Matches:
Conservative:
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Db 606 CAGAGCAATATGACTAGA 623

Search completed: July 30, 2005, 01:28:20 Job time: 224 secs

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Copyright

GenCore version 5.1.6 (c) 1993 - 2005 Compugen Ltd.

July 29, 2005, 22:49:43 ; Search time 716 Seconds (without alignments) 2766.119 Million cell updates/sec

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. (cgn2_6/ptodata/1/pubpna/USO8_NEW_PUB.Beq;*
. (cgn2_6/ptodata/1/pubpna/USO8_PUBCOMB.Beq;*
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. (cgn2_6/ptodata/1/pubpna/USO9A_PUBCOMB.Beq;*
. (cgn2_6/ptodata/1/pubpna/USO9A_PUBCOMB.Beq;*
. (cgn2_6/ptodata/1/pubpna/USO9A_PUBCOMB.Beq;*
. (cgn2_6/ptodata/1/pubpna/USOB_PUBCOMB.Beq;*
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score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

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20040107456A N: 20040107456A N: PLANT MYB 8919-088001 CON NUMBER: U YATE: 2003-07- 4 NUMBER: US 2002-07-31 NOS: 21 NOS: 21 PER WINDOWS		1136	1523	6 6 6 6 6 8	668	n 0 n 0 n 0	867	867	867	867	1793	1039	1021	1388	2481	1416	1363	1202	1140	1896	800	1432	1432	1432	965	2366	1523	1318	1516	1299	1330	918	Length
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		92,	56655,	J (4	2677,	249,	653,	2679,	653,	253,	183322	8016,	7450,	Sequence 52610, A	440,	Sequence 34322, A Sequence 52607, A	34323,	29755,	3444	1842	1139	863	18	35,	ដូដ		27578,	877	equence 2650, A	equence 168	quence 1, Appl	ce 4 Appl	Description

-MODEL=frame+ p2n.model -DEV=xlh
-Q=/cgn2 1/USPTO_spool/US10630636/runat_27072005_123229_12221/app_query.fasta_1.455
-Q=/cgn2 1/USPTO_spool/US10630636/runat_27072005_123229_12221/app_query.fasta_1.455
-DB=PublIshed_Applications_NA -QFMT=fastap -SUFFTX=rnpb -MINMATCH=0.1
-LOOPCL=0 -LOOPEXT=0 -UNITS=bits -START=1 -END=-1 -MATRIX=blosum62
-TRAMS=human40.cdi -LIST=45 -DOCALIGN=200 -THR SCORE=pct -THR MAX=100
-THR MIN=0 -ALIGN=15 -MODE=LOCAL -OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0
-MAXIEN=200000000 -USER=US10630636 @CGN 1 789 @runat 27072005 123229_12221
-NCPU=6 -ICPU=3 -NO_MMAP -LARGEQUERY -NEG_SCORES=0 -MAIT -DSPBLOCK=100
-LONGLOG -DEV_TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5
-FGAPOP=6 -FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Command line parameters:

Minimum DB seq length: Maximum DB seq length:

2000000000

Total number of hits satisfying chosen parameters:

14575566

7287783 seqs, 3236178273 residues

Searched:

Scoring table:

BLOSUM62

Xgapop 10.0 , Xgapext Ygapop 10.0 , Ygapext Fgapop 6.0 , Fgapext Delop 6.0 , Delext

0.5 7.0 7.0

Title: Perfect score:

US-10-630-636-7 1641

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GHAPYVVPVGYPAPPAKMHQ 306

Database :

Published_Applications_NA:*

/cgn2_6/ptodata/1/pubpna/US07_PUBCOMB.seq:*
/cgn2_6/ptodata/1/pubpna/PCT_NEW_PUB.seq:*
/cgn2_6/ptodata/1/pubpna/US06_PUBCOMB.seq:*
/cgn2_6/ptodata/1/pubpna/US06_PUBCOMB.seq:*

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Percent Similarity:
Best Local Similarity:
Query Match:
DB:
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; ORGANISM: Oryza sativa
US-10-630-636-4
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                                                          SerAlaAlaProMetGlyHisProValAlaGlyHisMetValProAlaAlaValGlyThr
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        ProValValPheProFroGlyHisAlaProTyrValValProValGlyTyrProAlaPro
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TITLE OF INVENTION: PLANT MYB GENES
FILE REFERENCE: 08919-088001
CURRENT APPLICATION NUMBER: US/10/630,636
CURRENT FILING DATE: 2003-07-30
PRIOR APPLICATION NUMBER: US 60/399,999
PRIOR FILING DATE: 2002-07-31
NUMBER OF SEQ ID NOS: 21
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 2
US-10-630-636-1
US-10-630-636-1
; Sequence 1, Application US/10630636
; Publication No. US20040107456A1
; GENERAL INFORMATION:
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Best Local Similarity:
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TYPE: DNA
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                                                        GlyIleProTrpThrGluGluHisArgLeuPheLeuLeuGlyLeuAspLysPheGly
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Sequence 59484, Application US/10437963

Publication No. US20040123343A1

Publication Youngedi

APPLICANT: Kovalic, David K.

APPLICANT: Wu, Wei

APPLICANT: Wu, Wei

APPLICANT: Boukharov, Andrey A.

APPLICANT: Barbazuk, Brad

APPLICANT: Barbazuk, Brad

APPLICANT: Li, Ping

TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With

TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement

FILE REFERENCE: 38-21(53221)B

CURRENT APPLICATION NUMBER: US/10/437,963

CURRENT APPLICATION NUMBER: US/10/437,963

CURRENT FILING DATE: 2003-05-14

NUMBER OF SEQ ID NOS: 204966

SEQ ID NO 59484

LENGTH: 1433

TYPE: DNA

ORGANISM: Oryza sativa

FEATURE:

OTHER INFORMATION: Clone ID: PAT_MRT4530_61102C.1

US-10-437-963-59484
                                                                                                                                            Percent Similarity:
Best Local Similarity:
Query Match:
DB:
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                                                           MetThrSerGlnAlaAlaThrThrThrThrThrAlaAlaAlaAlaAlaAlaAlaAlaTrpThrArg
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Sequence 168067 Application US/10425115

Publication No. US20040214272A1

GENERAL INFORMATION:
APPLICANT: La Rosa, Thomas J.
APPLICANT: Zhou, Yihua
APPLICANT: Zhou, Yihua
APPLICANT: Cao, Yongwei
TITLE OF INVENTION: Nucleic Acid Molecules a
TITLE OF INVENTION: Plants
FILE REFERENCE: 38-21(53222)B
CURRENT APPLICATION NUMBER: US/10/425,115
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 369326
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; TYPE: DNA
; CRGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: (
US-10-739-930-2650
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TITLE OF INVENTION: NUCLEIC ACID MOLECULES A
TITLE OF INVENTION: PLANTS AND USES THEREOF
FILE REFERENCE: 38-21(53377)B
CURRENT APPLICATION NUMBER: US/10/739,930
CURRENT FILING DATE: 2003-12-18
NUMBER OF SEQ ID NOS: 11088
SEQ ID NO 2650
LENGTH: 1516
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                                                                                                                                                               US-10-630-636-7 (1-306) x US-10-425-114-11058 (1-1281)
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US-10-425-114-11058
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LENGTH: 1281
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                                                                                                                                                                                                                                                                                                                                                                                                                                   TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement FILE REFERENCE: 38-21(53313)B
CURRENT APPLICATION NUMBER: US/10/425,114
CURRENT FILING DATE: 2003-04-28
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 73128
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APPLICANT: Zhou, Yihua
APPLICANT: Kovalic, Dav
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APPLICANT: Screen, Steven E
APPLICANT: Tabaska, Jack E
APPLICANT: Cao, Yongwei
                                                                                                                                                                                                                                                                                                                                                         TYPE: DNA
ORGANISM: Glycine
FEATURE:
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GENERAL INFORMATION:

APPLICANT: La Rosa Thomas J

APPLICANT: Kovalic David K

APPLICANT: Capalic David K

APPLICANT: Zhou Yihua

APPLICANT: Cao Yongwei

TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With

TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement

FILE REFERENCE: 38-21(53223)B

CURRENT APPLICATION UNMBER: US/10/424,599

CURRENT FILING DATE: 2003-04-28
                                                                                                                                                            Sequence 78776, Application US/10424599 Publication No. US20040031072A1
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; SEQ ID NO 78776
; LENGTH: 1318
; TYPE: DNA
; ORGANISM: Glycine (
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GlyGlyAlaProProMetProMetTyrSerAlaAlaProMetGlyHisProValAla
                                                         AsnProAlaAlaAlaAlaLeuGlyProProGlyMetLysHisHisHisHisHisHisPro
                                                                                                    AlaGlyAspGlnValAlaAlaGlnGlnGlyAlaProIleThrGlyHisGlnAlaThrGly
                                                                                                                                                                                     PheVallleSerArgThrProThrGlnValAlaSerHisAlaGlnLysTyrPheIleArg
                                                                                                                                                                                                                                                    LeuPheLeuLeuGlyLeuAspLysPheGlyLySGlyAspTrpArgSerIleSerArgAsn 170
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                                      ATTCCTTCAAACACAATGGGTGTAGGACAATCCCTTAAGCATAGAGTTCAGGGTCAC---
                                                                                                                                                      LeuAsnSerMetAsnArgAspArgArgArgSerSerIleHisAspIleThrSerValThr 210
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                                                                                                                                                                                                                                                                                                                                                                                                                                       GGTCACATATCATTCCCAAACTATGCTGCTTCTGAGGAAATCACATCTTCAAATAAGGAC
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; FEATURE:
; OTHER INFORMATION: Clone ID:
US-10-437-963-27578
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US-10-437-963-27578
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Best Local Similarity:
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APPLICANT: Li, Ping
APPLICANT: Li, Ping
APPLICANT: Li, Ping
TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21(53221)8
CURRENT APPLICATION NUMBER: US/10/437,963
CURRENT FILING DATE: 2003-05-14
NUMBER OF SEQ ID NOS: 204966
SEQ ID NO 27578
LENGTH: 1523
TYPET TIME APPLICATION PROBLEM TO THE PROBLEM TO
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APPLICANT: Kovalic, David K.
APPLICANT: Zhou, Yihua
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ORGANISM: Oryza sativa
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LysaspGlyGlyHisargArgAspGluArgLysGlyGlyGlyGlyGlyTyrAspGlyGly 128
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                                                                                                                                                                                                                                                                                                                                                             LeuValGluAspValAlaAlaIleAspAlaGlyArgValProLeuProArgTyrAlaGly
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                                                                                                                                                                                                                                                                                                            CTGGTGGAGGACGTCGACGGCATCGAGGCCGGGCGGGTGCCGCTTCCTGGTGTACGCCGGC 687
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Boukharov, Andrey
Barbazuk, Brad
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LOU, Yihua

APPLICANT: Kovalic, David K.

APPLICANT: Screen, Steven E

APPLICANT: Tabaska, Jack E

APPLICANT: Cao, Yongwei

TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associa

TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement

FILE REFERENCE: 38-21(5313))B

CURRENT APPLICATION NUMBER: US/10/425,114

CURRENT FILING DATS: 2003-04-28

NUMBER OF SEQ ID NOS: 73128

SEQ ID NO 4609

LENGTH: 823

TYPE: Dava
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 Alignment Scores: Pred. No.:
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APPLICANT: Kovalic David K
APPLICANT: Kovalic David K
APPLICANT: Cao Yongwei
TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21(5223)B
CURRENT APPLICATION NUMBER: US/10/424,599
CURRENT PILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 285684
SEQ ID NO 57473
LENGTH: 2366
                                                                                                                                                                                                                                                                                                                        Sequence 57473, Application US/10424599 Publication No. US20040031072A1 GENERAL INFORMATION:
                                                                                                         OTHER INFORMATION:
                                                                                                                                 TYPE: DNA
ORGANISM: Glycine max
                                                                                                                       FEATURE:
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RESULT 11
US-10-767-701-9031/c

(F. Sequence 9031, Application US/10767701
    Publication No. US20040172684A1
    GENERAL INFORMATION:
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US-10-630-636-7 (1-306) x US-10-767-701-9031 (1-965)
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APPLICANT: Zhou, Yihua
APPLICANT: Cao, Yongwei
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated
TITLE OF INVENTION: Plants and Uses Thereof For Plant Improvement
FILE REFERENCE: 38-21(53535)B
CURRENT APPLICATION NUMBER: US/10/767,701
CURRENT FILING DATE: 2004-01-29
NUMBER OF SEQ ID NOS: 63128
SEQ ID NO 9031
LENGTH: 965
TYPE: DNA
ORGANISM: Sorghum bicolor
FEATURE:
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                                                          ACAACA---ATTGGACAGCCAGTTGGTGGCCCTCTTGTC---TCAGCTGTTGGAACTCCT
                                                                                     AlaAlaProMetGlyHisProValAlaGlyHisMetValProAlaAlaValGlyThrPro
                                                                                                                                         AAACCATCTAAGCAATCCCCACAGCCAGCGAATACACCTCCAGGCGTCGATGCTTATGGC
                                                                                                                                                                            MetLysHisHisHisHisHisProGlyGlyAlaProProProMetProMetTyrSer
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APPLICANT: Zhou, Yihua

APPLICANT: Kovalic, David K.
APPLICANT: Screen, Steven E
APPLICANT: Tabaska, Jack E
APPLICANT: Tabaska, Jack E
APPLICANT: Cao, Yongwei
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION Plants and Uses Thereof for Plant Improvement
FILE REFERENCE 38-21(5313)B
CURRENT APPLICATION NUMBER: US/10/425,114
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NO 7669
SEQ ID NO 7669
LENGTH: 1230
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                                                                                                           GluArgLysGlyGlyGlyGlyTyrAspGlyGlyLysSerCysSerLysAlaGluGln
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CURRENT APPLICATION NUMBER: US/10/286,264
CURRENT FILING DATE: 2002-11-01
PRIOR APPLICATION NUMBER: 60/125,814
PRIOR FILING DATE: 1999-03-23
NUMBER OF SEQ ID NOS: 165
SOFTWARE: PATENTIN Ver. 2.1
SEQ ID NO 35
LENGTH: 1432
Alignment Scores: Score:
                                                               ; OTHER INFORMATION: US-10-286-264-35
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US-10-286-264-35
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TITLE OF INVENTION: POLYNUCLEOTIDES FOR SEED TRAIT ALTERATION
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                                                                                            TYPE: DNA ORGANISM: Arabidopsis thaliana FEATURE:
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Reuber, Lynne
Pilgrim, Marsha
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Jiang, Cai-Zhong
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Heard, Jacqueline
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Ratcliffe, Oliver
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No. US20030093837A1
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                                                                          ---ProVal---GlyTyrProAlaProProAlaLysMetHis 305
                                                                                                                              AlaValGlyThrProValValPhePro---ProGlyHisAlaProTyrValVal-----
                                                                                                                                                                                                                                     GGAGGAAACAAATCAGCCAAG------CAAGCCGTCTCTCAAGCACCACCTGGA
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                                                                                                          GCAGTTGGAACACCAGTGAACCTCCCAGCTCCACCTCACATGGCTTATGGAGTTCATGCG
                                                                                                                                                                      CCTCCTATGTATGGAACACCCGCCATAGGTCAGCCA-----
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APPLICANT: Broun, Pierre
TITLE OF INVENTION: STRESS-INDUCED POLYNUCLEOTIDES
FILE REFERENCE: MBI-011
CURRENT APPLICATION NUMBER: US/10/278,536
CURRENT FILING DATE: 2002-10-22
PRIOR APPLICATION NUMBER: 60/125,814
PRIOR FILING DATE: 1999-03-23
NUMBER OF SEQ ID NOS: 238
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 187
LENGTH: 1432
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Publication No. US20030131386A1
GENERAL INFORMATION:
APPLICANT: Samaha, Raymond
APPLICANT: Heard, Jacqueline
APPLICANT: Heard, Jacqueline
APPLICANT: Pineda, Omaira
APPLICANT: Pineda, Omaira
APPLICANT: Reuber, Lynne
APPLICANT: Rechmann, Jose-Luis
APPLICANT: Wi, Guo-Liang
APPLICANT: Keddie, James
APPLICANT: Keddie, James
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DB:
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US-10-278-536-187
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Reuber, Lynne
Riechmann, Jose-Luis
Yu, Guo-Liang
Yu, Guo-Liang
Keddie, James
Ratcliffe, Oliver
Pilgrim, Marsha
                                                                          GluGluHisArgLeuPheLeuClyLeuAspLysPheGlyLysGlyAspTrpArgSer 166
                                                                                                                                                                                                     GCCTATGGGTCTCCTGAAGGATCG------AATGGCCATGCTGATGAAGGAGCA
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                 GATGAGCACAGGTTATTTCTTCTTGGTTTGGATAAGTACGGGAAAGGTGATTGGCGTAGC
                                                                                                                                         AGTAGTAAGAAAGGAGGTAACAGTCAT--------GCGGGAGAGTCTAACCAA
                                                                                                                                                                   AlaSerLysAspGlyGlyHisArgArgAspGluArgLysGlyGlyGlyGlyTyrAsp
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Gaps:
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Matches:
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RESULT 15
US-10-302-267-157
Sequence 157, Applicat
Publication No. US2003
GENERAL INFORMATION:
CURRENT APPLICATION NUMBER: US/10/302,267
CURRENT FILING DATE: 2002-11-22
PRIOR APPLICATION NUMBER: US/09/506,720
PRIOR FILING DATE: 2000-02-17
PRIOR PPLICATION NUMBER: 60/120,880
PRIOR PPLICATION NUMBER: 60/120,880
PRIOR APPLICATION NUMBER: 60/121,037
PRIOR APPLICATION NUMBER: 60/121,037
PRIOR FILLING DATE: 1999-03-21
PRIOR APPLICATION NUMBER: 60/124,278
PRIOR FILLING DATE: 1999-03-11
PRIOR PPLICATION NUMBER: 60/129,450
PRIOR FILLING DATE: 1999-04-15
PRIOR APPLICATION NUMBER: 60/135,134
PRIOR APPLICATION NUMBER: 60/14,153
PRIOR PILLING DATE: 1999-07-15
PRIOR PPLICATION NUMBER: 60/14,153
PRIOR PILLING DATE: 1999-07-15
PRIOR APPLICATION NUMBER: 60/161,143
PRIOR APPLICATION NUMBER: 60/161,143
PRIOR APPLICATION NUMBER: 60/161,143
PRIOR APPLICATION NUMBER: 60/161,143
PRIOR APPLICATION NUMBER: 60/162,656
PRIOR FILLING DATE: 1999-10-22
PRIOR APPLICATION NUMBER: 60/162,656
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APPLICANT: Pineda, Omaira
APPLICANT: Reuber, Lynne
APPLICANT: Zhang, James
APPLICANT: Yu, Guo-Liang
APPLICANT: Jiang, Cai-Zhong
APPLICANT: Samaha, Raymond
APPLICANT: Samaha, Raymond
APPLICANT: Creelman, Marsha
APPLICANT: Creelman, Robert
TITLE OF INVENTION: PLANT GENE SEQUENCES II
FILE REFERENCE: MBI-0007
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Keddie, James
APPLICANT: Fromm, Michael
APPLICANT: Heard, Jacquel
APPLICANT: Riechmann, Jos
APPLICANT: Adam, Luc
APPLICANT: Broun, Pierre
APPLICANT: Reuber, Lynne
APPLICANT: Reuber, Lynne
APPLICANT: Yu, Guo-Liang
APPLICANT: Yu, Guo-Liang
APPLICANT: Yu, Guo-Liang
APPLICANT: Samaha, Raymon
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; NAME/KEY: CDS
; LOCATION: (259)..(11
; OTHER INFORMATION: G
US-10-302-267-157
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SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 157
LENGTH: 1432
TYPE: DNA
ORGANISM: Arabidopsis thaliana
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                                    LeuGlyProProGlyMetLysHisHisHisHisHisHisProGlyGlyAlaProProPro
                                                                                                                                                                                                                                                             TyrPheIleArgLeuAsnSerMetAsnArgAspArgArgArgSerSerIleHisAspIle
                                                                                                                                                                                                                                                                                                                                          IleSerArgAsnPheValIleSerArgThrProThrGlnValAlaSerHisAlaGlnLys
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                                                                                     AACAACAGCAATAACAACAACAACAACAACAACAACAACAGTTCTCCTGCTGTTGCTGGA
                                                                                                                       GlnAlaThrGlyAsn-----
                                                                                                                                                                                                  ThrSerValThrAlaGlyAspGlnValAlaAlaGlnGlnGlyAlaProIleThrGlyHis
                                                                                                                                                                                                                                                                                                                      ATTTCTCGCAACTTTGTAGTAACAAGAACACCGACCCAAGTTGCGAGCCATGCTCAAAAG
                                                                                                                                                              ACTAGTGTTGGCAACGCAGATGTCTCAACCGCCACAAGG-----CCAATCACTGGTCAG
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38.06%
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Matches:
Conservative:
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Indels:
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          -CAAGCCGTCTCTCAAGCACCACCTGGA
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Search Job ti	ф	Qy	ф	Qy	Дb	Ş
Search completed: Job time: 729 secs	1063	294	1003	277	967	257
Search completed: July 30, 2005, 01:40:17 Job time : 729 secs	1063 GCTCCAGTCCTGGCTCAGTGGTTCCTGGTGCAGCAATGAAC 1104	ProValGlyTyrProAlaProProAlaLysMetHis 305	1003 GCAGTTGGAACACCAGTGAACCTCCCAGCTCCACATGGCTTATGGAGTTCATGCG 1062	277 AlaValGlyThrProValValPheProProGlyHisAlaProTyrValVal 293	967 CCTCCTATGTATGGAACACCCGCCATAGGTCAGCCA 1002	257 MetProMetTyrSerAlaAlaProMetGlyHisProValAlaGlyHisMetValProAla 276

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Title:
Perfect score:
Sequence:
                                                                                                                                                                                                                                                                                                                                    Result
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-DB=EST -OPMT=fastap -SUFFIX=rst -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0
-UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45
-DCCALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALICN=15 -MODE=LOCAL
-OUTFMT=pto -NORM=ext -HEAPSIZE=50 -MINLEN=0 -MAXLEN=200000000
-USER=US10630636 @CGN 1 1 4352 @runat 2707205 123227 12178 -NCPU=6 -ICPU=3
-NO_MMAP -LARGEQUERY -NEG_SCORES=0 -MIT -DSPBLOCK=100 -LOGLOG
-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -PGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPOEXT=0.5 -DELOP=6 -DELEXT=7
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Maximum Match 100%
Listing first 45 summaries
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Maximum DB seq length: 200000000
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-MODEL=frame+_p2n.model
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Searched:
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      828.5
816.5
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787.5
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737
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1641
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Ygapop 10.0 , Ygapext
Fgapop 6.0 , Fgapext
Delop 6.0 , Delext
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CG257740
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                      GG257740 OGXCQ48TH
BQ483926 WHB3514 C
CF326660 JMT1-06-
B2525067 OGAHT80TC
CA185031 SCSBST309
CG362076 OG1CL41TH
CK256709 EST740346
CK254513 EST738150
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σ o ~	J 57	7762	5 7 7	9 1 9 1	9739	997	97876	9977777
CB001319 CB002201	CO119900 BQ864479	BE433827 CA233892 CO081265 CF450963	CK257718 CK259272 BU025086	BE356185 CA243768 CO121658 CB003696	CC751932 CNSOA13X CK290192 CC752461	CV500657 CG366978 CG219911	CNS0A16S CO089242 CNS0A0SA CK258863 CC710311	CK294026 CO082313 CK248989 CK292080 CK259271 CK2597717 CC257748 CG219919
CB001319 VVB005F12 CB002201 VVB014A12	CO119900 GR Eb023 BQ864479 QGC26N06.	EST40490 SCSGFL4C GR Ea45 EST68730	CK257718 EST741355 CK259272 EST742909 BU025086 QHF7J19.y	DG1 123 SCQGFL40 GR Eb02 VVB03280	CC751932 ZMMBBb013 BX832663 Arabidops CK290192 EST752914 CC752461 ZMMBBb013		EX832500 Arabidops CO089242 GR Ea08K BX831116 Arabidops CK258863 EST742500 CC710311 OGDAH26TC	94026 82313 48989 92080 9271 59271 57717 57748

## ALIGNMENTS

	source	FEATURES									COMMENT	JOURNAL	TITLE			AUTHORS	REFERENCE				ORGANISM	SOURCE	KEYWORDS	VERSION	ACCESSION		DEFINITION	Locus	CG257740/c	RESULT 1
/organism="Zea mays" /mol_type="genomic DNA" /strain="B73"	1 884	Location/Qualifiers	Class: sheared ends.	Seq primer: TR	Email: whitelaw@tigr.org	Fax: 301-838-0208	Tel: 301-838-5843	9712 Medical Center Drive, Rockville, MD 20850, USA	TIGR	Contact: Cathy Whitelaw	Other_GSSs: OGXCQ48TV	Unpublished (2002)	Consortium for Maize Genomics	Citek, R.W., Numberg, A., Robbins, D. and Lakey, N.	Resnick, A., Fraser, C.M., Budiman, M.A., Bedell, J.A., Rohlfing, T.,	Whitelaw, C.A., Quackenbush, J., Van Aken, S., Utterback, T.,	1 (bases 1 to 884)	clade; Panicoideae; Andropogoneae; Zea.	Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;	Zea mays	Zea mays	GSS.	CG257740.1 GI:34164524	CG257740	genomic survey sequence.	OGXCQ48TH ZM_0.7_1.5_KB Zea mays genomic clone ZMMBMa0650G23,	CG257740 884 bp DNA linear GSS 25-AUG-2003		

CK251993

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RESULT 2
BQ483926
LOCUS
    DEFINITION
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BQ483926
WHE3514_C07_E14ZS
                                                                                    GlyTyrProAlaProProAlaLysMetHisGln 306
                                                                                                                                                                               GGCATGTACGGGCACGCGCCCATGGGCCACCCGGTCTCGGGGCACATGGTGGCGCCGGCG
                                                                                                                                                                                               ProMetTyrSerAlaAlaProMetGlyHisProValAlaGlyHisMetVal----
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/clone="ZMMBMA0650623"
/clone_lib="ZM_0.7_1.5KB"
/note="Vector: pBCSK-; Site_1: HincII; 0.7-1.5
methylation filtered genomic DNA library"
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1 (bases 1 to 689)

Anderson,O.D., Chao,S., Close,T.J., Crossman,C., Fenton,R.D.,
Lazo,G.R., Nguyen,H.T., Rausch,C.J., Wilson,C., Woo,J. and Zhang,
The structure and function of the expressed portion of the wheat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          aestivum cDNA clone WHE3514_C07_E14,
BQ483926
BQ483926.1 GI:21319862
EST.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Email: oandersn@pw.usda.gov
Sequences have been trimmed
quality sequence with phred
Seq primer: SK primer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            800 Buchanan Street, Albany, CA 94710, USA Tel: 5105595773
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Unpublished (2002)
Contact: Olin Anderson
US Department of Agriculture, Agriculture Research
West Area, Western Regional Research Center
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Fax: 5105595818
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Spermatophyta; Magnoliophyta; Liliopsida; Pooideae; Triticeae; Triticum.
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Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
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SerAlaGluGluValArgArgHisTyrGluAlaLeuValGluAspValAlaAlaIleAsp
                                                                                                     GlyGlyAlaProAspAspAspTrpPheAlaAlaLeuAlaAlaSerValProGlyAlaArg
                                                                                                                                                                                                       GluAspAspLysAlaPheGluAsnAlaLeuAlaAlaCysAlaAlaProProProAlaAsp
                                                                                                                                                                                                                                                                          --- GCCGTGCCGGAGGAGTGCTGGTTCGCGGCGCCTCGCGGCGAGCGTGCCG---GCGCGG
                                                                                                                                                               GAGGAGGACAAGGCGTTCGAGAACGCGGTCGCATCC---GGTGCACCGCCGCCGCTGGAC
                                                                                                                                                                                                                                                     ATGCCTCTCAGGGAGCGACCACG-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /Clone_lib="Wheat unstressed root cDNA library"
//clone="Vector: Lambda Uni-ZAP XR, excised phagemid
/note="Vector: Lambda Uni-ZAP XR, excised phagemid
pBluescript SK(-); Site_1: EcoR; Site_2: XhoI; Plants
were grown until full tillering stage and root tissue was
collected at Texas Tech Univeristy (Zhang, HT Nguyen
Lab). Total RNA and poly(A) RNA were prepared, a cDNA
library was made, and the cDNA clones were in vivo
excised to give pBluescript SK(-) phagemids in the TJ
Close lab (Close, Fenton) at the University of
California, Riverside. Colony plating, plasmid DNA
preparations and DNA sequencing were performed in the OD
Anderson lab (all other authors)."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /db_xref="taxon:4565"
/clone="wHE3514 C07 E14"
/tissue_type="Roots"
/dev_stage="Fill tillering"
/lab_host="E. coli SOLR"
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/cultivar="Chinese
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1 (bases 1 to 478)

Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
                                                                                                                                                                                                                                                                    Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
                                                                                                                                                                                                                                                                                                                                                   478 bp mRNA linear EST 18 MT1--06-K20.gl AtJMT-overexpressing transgenic rice lambda cDNA library (JMT1) Oryza sativa (japonica cultivar-group) clone JMT1--06-K20, mRNA sequence.
                                                                                                                        Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, MyongJi University Yongin, Kyeonggi, Korea Tel: 82 31 330 6193 Fax: 82 31 321 6355
                                                                                                                                                                                                                                                                                                                                     CF326660
CF326660.1
                                                                                                                                                                                       Contact: Nahm B.H.
                                                                                                                                                                                                  Large-scale Sequencing Analysis 
Unpublished (2003)
                                                                                                                                                                                                                                                              Ehrhartoideae; Oryzeae; Oryza.
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                                                                                                               bhnahm@ggbio.com,
                                   /organism="Oryza sativa
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/clone="JMT1--06-K20"
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/clone_lib="AtJMT-overexpressing transgenic rice lambda
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/clone_lib="AtJMT-overexpression line."
/clone_lib="AtJMT-overexpression line."
/clone_lib="AtJMT-overexpression line."
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US-10-630-636-7 (1-306) x CF326660
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1 (bases 1 to 759)
Whitelaw, C.A., Quackenbush, J., Van Aken, S.
Resnick, A., Fraser, C.M., Budiman, M.A., Bed
Citek, R.W., Numberg, A., Robbins, D. and Lak
Consortium for Maize Genomics
Unpublished (2002)
Contact: Cathy Whitelaw
TIGR
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Zea mays
Zea mays
Eukaryota;
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methylation filtered genomic DNA library"
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Caixa Postal 6010, 13083-970, Camp
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Contact: Arruda P
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Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
clade; Panicoideae; Andropogoneae; Saccharum; Saccharum officinaru
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Seq primer: T7 Promoter Primer.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Email: parruda@unicamp.br
Clone distribution: clone distribution
through the Brazilian Clone Collection
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The libraries that made SUCEST
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/lab_host="DH10B"
/clone_lib="ST3"
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/mol_type="mRNA"
/db_xref="taxon:4547"
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              Medical Center Drive,
301-838-5843
301-838-0208
 whitelaw@tigr.org
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/clone_lib="ZM_0.7_1.5_KB"
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Buell, C.R., Hart, A., Zismann, V., Karamycheva, S.A. and Baker, B. Generation of ESTs from potato callus tissue Unpublished (2003)

Contact: Robin Buell

The Institute for Genomic Research

9712 Medical Center Dr, Rockville, MD 20850, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EST740346 potato callus cDNA
Solanum tuberosum cDNA clone
CK256709
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Solanum tuberosum
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Seq primer: ATT TAG GTG ACA CTA TAG.
Location/Qualifiers
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Clones can be requested from the University of Arizona Genomics
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                                           LeuProArgTyrAlaGlyGluGlu---SerAlaAlaProProAspGlyAlaGlyAlaAla 104
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                                                                                                                                                                                                                                                                                                  TCATCTTCAGTAGTGTGGAGCAGAGAAGAAGAAAAAGCTTTTGAGAATGCCATTGCTCTG
                   ATACCCAATTACAAAGGAGAAGAAGCTTCTTCCTTTCAACTAAAGAAGTTAATCTAGGA 315
                                                                                                                                                                                                                                                              CysAlaAlaProProAlaAspGlyGlyAlaProAspAspAspTrp------
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supplier: RNA was isolated from Solanum tuberosum var.
Kennebec callus tissue grown on solid media."
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/lab_host="DH10B-TonA"
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/clone="POCCV46"
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/cultivar="Kennebec"
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library, normalized and full-length
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
asterids; lamids; Solanales; Solanaceae; Solanum.
1 (bases 1 to 973)
Buell, C.R., Hart, A., Zismann, V., Karamycheva, S.A. and Baker, B.
Generation of ESTs from potato callus tissue
                                                                                                                       Unpublished (2003)
Other_ESTs: EST738151
                                                                                                                                                                                                                                                                                                                                                 CK254513

EST738150 potato callus cDNA Solanum tuberosum cDNA clone
 Email: potato-array@tigr.org
Clones can be requested from the University of Arizona
Institute via http://genome.arizona.edu/orders/.
Seq primer: ATT TAG GTG ACA CTA TAG.
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Solanum tuberosum (potato)
                                                                    The Institute for Genomic Research 9712 Medical Center Dr, Rockville,
                                                                                                          Contact: Robin Buell
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primer:
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Best Local Similarity:
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TCAACTCATCAA---GCTCCAATTACAGGCCAACAGGTGAATCCGAATCCATCAAATCCA
           AlaAlaGlnGlnGlyAlaProIleThrGlyHisGlnAlaThrGlyAsnProAla---Ala
                                                AGAGATAGAAGGAGGTATTCACGACATTACAAGTATCAATAATGGAGGAGACGTT
                                                               ArgAspArgArgArgSerSerIleHisAspIleThrSerValThrAlaGlyAspGlnVal
                                                                                                 ACACCAACACAAGTAGCTAGTCATGCCCAGAAATACTTTATTCGTTTGAATTCCATGAAT
                                                                                                                 ThrProThrGlnValAlaSerHisAlaGlnLysTyrPheIleArgLeuAsnSerMetAsn
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supplier: RNA was isolated from Solanum tuberosum var.
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/mol_type="mRNA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        full-length"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /tissue_type="callus"
/lab_host="DH10B-TonA"
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/clone="POCCD92"
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EST735630 potato callus cDNA library, no
Solanum tuberosum cDNA clone POCBR77 5'
CK251993
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Contact: Robin Buell
The Institute for Genomic Research
9712 Medical Center Dr, Rockville,
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Buell, C.R., Hart, A., Zismann, V., Karamycheva, S.A.
Generation of ESTs from potato callus tissue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Email: potato-array@tigr.org
Clones can be requested from the University of Arizona Genomics
Institute via http://genome.arizona.edu/orders/ .
Seq primer: ATT TAG GTG ACA CTA TAG.
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AlaAlaAlaAlaAlaTrpThrArgGluAspAspLysAlaPheGluAsnAlaLeuAlaAla
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supplier: RNA was isolated from Solanum tuberosum var.
                                                                                                                                                                                                                                        Kennebec callus tissue grown
                                                                                                                                                                                                                                                                                         full-length"
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/cultivar="Kennebec"
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                                                                                                                                                                                                                                                                                                       clone_lib="potato callus cDNA library, normalized and
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Clones can be requested from the University of Arizona Institute via http://genome.arizona.edu/orders/ . Seq primer: ATT TAG GTG ACA CTA TAG.
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Other_ESTs: EST756741
Contact: Robin_Buell
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1 (bases 1 to 952)
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                                              AlaAlaAlaAlaAlaSerLysAspGlyGlyHisArgArgAspGluArgLysGlyGlyGly 122
                                                                                                        AATGTTCCAATTCCAATATACACAGAAGAGGAA----
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/lab_host="DH10B-TonA"
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/mol_type="mRNA"
/db_xref="taxon:4100"
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                                                                       Arizona Genomics Institute
Arizona Genomics Institute
The University of Arizona
Forbes Building Room 303, Tucson, AZ, 8:
Tel: 520 626 9595
Fax: 520 621 1259
Email: http://genome.arizona.edu
Plate: 46 row: N column: 19.
Location/Qualifiers
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Contact: Rod A. Wing
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Eparmatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
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Kim, H., Yu, Y., Kudrna, D., Hatfield, J., Stum, D., Mueller, C.,
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                       GCAGCGGTCATGGGG----CAATCAGTGAAGCACAGGGCTCAGCCGCAT--
                                                                                                                                                                                  AATAGAGACCGGCGGCGGTCCAGCATCCACGACATCACGAGTGTTAACAATGGGGAT---
                                                                                                                                                                                                                                                                 AGAACTCCGACGCAGGTGGCTAGCCATGCACAAAAGTATTTTATACGCTTAAATTCGATG
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/lab_host="DH10B"
/clone lib="GR Ea"
/clone lib="GR Ea"
/clone lib="GR Ea"
/clone lib="GR Ea"
/clone lib="DCMV.SPORT-6.1; Site 1: NotI; Site 2:
/note="Vector: DCMV.SPORT-6.1; Site 1: NotI; Site 2: NotI; Site 1: NotI; Site 2:
/note="Vector: DCMV.SPORT-6.1; Site 1: NotI; Site 2: NotI; Site 2: NotI; Site 1: NotI; Site 2: NotI; Site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /clone="GR_Ea46N19"
/tissue_type="whole seedlings"
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713.50
63.82%
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661 233 607 214 550 194 490 174 154

430

134

310

370

103

85 142 65 88 \$ 61 31

202

Alignment Scores: Pred. No.:  694.50  Acches: Fred. No.:  694.50  Matches:  158  Conservative:  32  Best Local Similarity:  42.32*  Mismatches:  57  Query Match:  7  Gaps:  US-10-630-636-7 (1-306) x CK248989 (1-921)  Qy  13 AlaAlaAlaAlaAlaTrpThrArgGluAspAspLysAlaPheGluAsnAlaLeuAlaAla 32  ::::::::  Db  105 TCATCTTCAGTAGTGGAGCAGAAGAAGAAAAAGCTTTTGAGAATGCCATTGCTCTG  Qy  33 CysAlaAlaProProProAlaAspGlyGlyAlaProAspAspAspAspTrp	Seq primer: ATT TAG GTG ACA CTA TAG.  FEATURES: Location/Qualifiers  1. 921  /organism="Solanum tuberosum" /mol_type="mRNA" /cloine="pocB507" /tissue_type="callus" /lob_hoset="PHOEB-TONA" /cloine_lib="potato callus cDNA library, normalized and full-length" /note="vector: pCMVSport6.1; Site_1: BcoRI; Site_2: NotI; supplier: RNA was isolated from Solanum tuberosum var. Kennebec callus tissue grown on solid media."	Eukaryota; Viridiplantae; Etreptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids; lamiids; Solanales; Solanaceae; Solanum.  REFERENCE 1 (bases 1 to 921)  AUTHORS Buell, C.R., Hart, A., Zismann, V., Karamycheva, S.A. and Baker, B.  TITLE Generation of ESTS from potato callus tissue  Unpublished (2003)  Other ESTS: EST732627  COMMENT Contact: Robin Buell  The Institute for Genomic Research  9712 Medical Center Dr, Rockville, MD 20850, USA  Email: potato-array@tigr.org  Clones can be requested from the University of Arizona Genomics	RESULT 12 CK248989 CK248989 CK248989 CK248989 CK248989 CK248989 DEFINITION CK248989 CK248989 CK248989 CK248989 CK248989 CK248989 CK248989 CK248989 CK248989.1 GI:39799665 SOURCE Solanum tuberosum (potato) ORGANISM Solanum tuberosum	Qy 254 ProProProMetProMetTyrSerAlaAlaProMetGlyHisProValAla 270
CK292080  CK292080  CK292080  DEFINITION  EST754794 Nicotiana benthamiana mixed tissue cDNA library, normalized, full-length Nicotiana benthamiana cDNA clone NBMC676 5', end, mRNA sequence.  CK292080  VERSION  CK292080  CK292080.1 GI:39873168  EST7.  SOURCE  ORGANISM  Nicotiana benthamiana  CNGANISM  Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids; lamiids; Solanales; Solanaceae; Nicotiana.  1 (bases 1 to 938)  BUILIC: R., Hart, A., Zismann, V., Karamycheva, S.A., Day, B., Staekawicz, B., Jin, H. and Baker, B.  TITLE  JOURNAL Generation of EST sequences from Nicotiana benthamiana  Unpublished (2003)  Other_EST8: EST754795  Contact: Robin Buell  The Institute for Genomic Research  9712 Medical Center Dr, Rockville, MD 20850, USA	Db 711 TCAACTCATCAA	Qy 156 LeuAspLysPheGlyLysGlyAspTrpArgSer1leSerArgAsnPheValIleSerArg	360 TATCCTGGGTCAGTGACGGACGGCGCTCCAATTGTGGTTATTCAAATGGA  125 TyrAsp	Db 183 GAACAGCAATGGGAGCAGTTTGCTTCTATGGTCCCCACAAAGACCATTGATGAGCTT 239  66 ArgArgHisTyrGluAlaLeuValGluAspValAlaAlaIleAspAlaGlyArgValPro 85  210 AAGGACATTACCAGCTACTTTTTGGAAAGATGCATTGAAGCAGGCCAAGTTCCA 299  86 LeuProArgTyrAlaGlyGluGluSerAlaAlaProProAspGlyAlaGlyAlaAla 104  21

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Best Local Similarity:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          30 LeuAlaAlaCysAlaAlaProProProAlaAspGlyGlyAlaProAspAspAspTrp---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Clones can be requested from the University of Arizona Genomics Institute via http://genome.arizona.edu/orders/ . Seq primer: ATT TAG GTG ACA CTA TAG.
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CATAGGTTTTTCTTGCTTGGTTTAGATAAGTTCGGAAAGGGAGACTGGAGAAGTATTTCA
                   HisArgLeuPheLeuLeuGlyLeuAspLysPheGlyLysGlyAspTrpArgSerIleSer 168
                                                                       AAAGGAAGTTCCAAATCTGAAAACGAAAGAAAAGGAAAACGAATACCTTGGACTGAAGAAGAA
                                                                                                                                                   TCTTTTTGTAGTTATGTAAATGGATTTTCAGGTAGTGTACATGAAATTGGCCAAGGAGGA
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                                                                                                                                                                                                                                                                                                       AATGTTCCAATTCCAATATACACAGAAGAGGAA-----
                                                                                                                                                                                                                                                                                                                                           ArgValProLeuProArgTyrAlaGlyGluGluSerAlaAlaProProAspGlyAlaGly 102
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                                                                                                   LysSerCysSerLysAlaGluGlnGluArgArgLysGlyIleProTrpThrGluGluGlu
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          clone_lib="Nicotiana benthamiana mixed tissue cDNA library, normalized, full-length"

/note="Vector: pCNVSport6.1; Site 1: EcoRI; Site 2: NotI; supplier: RNA was isolated from NIcotiana benthamiana tissues that include callus, roots from liquid culture grown plants, heat-stressed leaves (38 C, 3 hr and 6 hr), cold-stressed leaves (5 C 3 hr, 6hr), and pathogen challenged leaves (5 C 3 hr, 6hr), and pathogen challenged leaves (Pseudomonas syringae pv tomato 12 hr; Beaudomonas syringae pv phaseolicola 18hr, and Xanthomonas campestris pv campestris 12 hr, 18hr; Beaudomonas syringae pv phaseolicola 18hr, and Xanthomonas campestris pv vegicatoria 18hr). RNA was isolated from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /tissue_type="abiotic and biot
callus tissue and root tissue"
/lab_host="DH10B-TonA"
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|mol_type="mRNA"
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664.50
62.13*
49.83*
40.49*
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                                                                                                                                                                                       -GlyGlyTyr---
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Alignment
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ORGANISM
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Solanum tuberosum (potato)
Solanum tuberosum
Solanum tuberosum
Solanum tuberosum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Core eudicots;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Spermatophyta; Magnoliophyta; Solanaceae; Solanum.
                                                                                                                                                                                                                                                                                                                                                                                                The Institute for Genomic Research 9712 Medical Center Dr. Rockville, Email: potato-array@tlgr.org
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Unpublished (2003)
Other_ESTs: EST742909
Contact: Robin Buell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Spermatophyta; Magnoliophyta; eudicotyledons; coreasterids; lamiids; Solanales; Solanaceae; Solanum. 1 (bases 1 to 956)
Buell, C.R., Hart, A., Zismann, V., Karamycheva, S.A. Generation of ESTs from potato callus tissue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CK259271 956 bp mRNA linear EST 30-JUL-2004 EST742908 potato callus cDNA library, normalized and full-length Solanum tuberosum cDNA clone POCDN73 5' end, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                           Clones can be requested from the University of Arizona Institute via http://genome.arizona.edu/orders/ . Seg primer: ATT TAG GTG ACA CTA TAG.
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                                                                                       /note="Vector: pCMVSport6.1; Site_1: EcoRI; Site_2: NotI; supplier: RNA was isolated from Solanum tuberosum var. Kennebec callus tissue grown on solid media."
                                                                                                                                                                                                                                 /organism="Solanum tuberosum"
/mol_type="mRNA"
/cultivar="Kennebec"
/db_xref="taxon:4113"
                                                                                                                                                                                /tissue_type="callus"
/lab_host="DH10B-TonA"
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                                                                                                                                                             clone_lib="potato callus cDNA library, normalized
                                                                                                                                                                                                                    clone="POCDN73"
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  Solanum tuberosum Solanum tuberosum
                                               CK257717 961 bp mRNA linear BST 30-JUL-2004 EST741354 potato callus cDNA library, normalized and full-length Solanum tuberosum cDNA clone POCD756 5' end, mRNA sequence. CK257717
                                     CK257717.1 GI:39814697
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TCATCTTCAGTAGTGGGAGCAGAGAAGAAGAAAAGCTTTTGAGAATGCCATTGCTCTG
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1 (bases 1 to 961)
Buell, C.R., Hart, A., Zismann, V., Karamycheva, S.A. and Baker, B. Generation of ESTs from potato callus tissue Unpublished (2003)
Other_ESTs: EST741355
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Email: potato-array@tigr.org
Clones can be requested from the University of Arizona
Institute via http://genome.arizona.edu/orders/ .
Seq primer: ATT TAG GTG ACA CTA TAG.
Location/Qualifiers
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GlnGluArgArgLysGlyIleProTrpThrGluGluGluHisArgLeuPheLeuLeuGly
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GAACAGCAATGGGAGCAGTTTGCTTCTATGGTCCCC---ACAAAGACCATTGATGAGCTT
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                                                             TTTTCAGGTACGACCCATGACCCGATTGGGCATGGTGGAAAAGGGGAATTCTAGGTCTGAA
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/mol_type="mRNA"
/cultivar="Kennebec"
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/lab_host="DH10B-TonA"
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/clone="POCD756"
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Qy 216 AlaAlaGInGInGlyAlaProIleThrGlyHisGInAlaThrGlyAsnProAlaAla :::
Qy 196 ArgAspArgArgSerSerIleHigAspIleThrSerValThrAlaGlyAspGlnVal
176 683
Qy 156 LeuasplysPheGlyLysGlyAspTrpArgSerIleSerArgAsnPheVallieSerArg

Search completed: July 30, 2005, 01:24:41 Job time: 3698 secs

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